



SEQUENCE LISTING

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<120> Fusion Proteins of Mycobacterium Tuberculosis

<130> 014058-009041US

<140> US 09/688,672

<141> 2000-10-10

<150> US 60/158,338

<151> 1999-10-07

<150> US 60/158,425

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<160> 202

<170> PatentIn Ver. 2.1

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<213> Mycobacterium tuberculosis

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<223> Mtb81

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Ser Phe Trp Ala Gly Val Asp Lys Val Val Ala Asp Leu Thr Pro Gln
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Lys Trp His Arg Arg Arg Val Ile Glu Pro Ile Asp Met Asp Ala Tyr
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Arg Gln Phe Leu Thr Glu Ile Gly Tyr Leu Leu Pro Glu Pro Asp Asp
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Thr Met Lys Ser Gln Pro Trp Ile Leu Ala Tyr Glu Asp His Asn Val	
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625 630 635 640	
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 <213> Mycobacterium tuberculosis

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 595 600 605
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 His Asp Val Ala Leu Met Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser
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 Thr Pro Gly Arg Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu
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 Gly Tyr Ala Ala Lys Val Phe Arg Ala Val Ala Arg Arg Arg Arg Gln
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 tggcaatttc ttgttgcccg acgcgcaaag cattcaggcc gcggcggtcg gcttcgcctc 1020
 gaaaaccccc gcgaaccagg cgatttcgat gatcgacggg cccgccccgg acggctaccc 1080
 gatcatcaac tacgagtacg ccatcgctcaa caaccggcaa aaggacgccg ccaccgcgca 1140
 gaccttgacg gcatttctgc actgggcatg caccgacggc aacaaggcct cgttcctcga 1200
 ccaggttcat ttccagccgc tgccgcccgc ggtggtgaag ttgtctgacg cgttgatcgc 1260
 gacgatttcc agctagcctc gttgaccacc acgcgacagc aacctccgtc gggccatcgg 1320

```

gctgctttgc ggagcatgct ggcccgtgcc ggtgaagtcg gccgcgctgg cccggccatc 1380
cgggtggttg gtgggatagg tgcggtgatc ccgctgcttg cgctggtctt ggtgctggtg 1440
gtgctggtca tcgaggcgat ggggtgcgatc aggctcaacg ggttgcatth cttcaccgcc 1500
accgaatgga atccaggcaa cacctacggc gaaaccgttg tcaccgacgc gtcgcccac 1560
cggtcggcgc ctactacggg gcgttgccgc tgatcgctcg gacgctggcg acctcgga 1620
tcgccctgat catcgcggtg ccggtctctg taggagcggc gctgggtgatc gtggaacggc 1680
tgccgaaacg gttggccgag gctgtgggaa tagtcctgga attgctcgcc ggaatcccc 1740
gcgtggtcgt cggtttggg ggggcaatga cgttcgggcc gttcatcgct catcacatcg 1800
ctccggtgat cgctcacaac gctcccgatg tgccggtgct gaactacttg cgcggcgacc 1860
cgggcaacgg ggagggcatg ttggtgtccg gtctggtgtt ggcggtgatg gtcgttcccc 1920
ttatcgccac caccatcat gacctgttcc ggcaggtgcc ggtgttgccc cgggagggcg 1980
cgatcgggaa ttc
1993

```

```

<210> 8
<211> 374
<212> PRT
<213> Mycobacterium tuberculosis

```

```

<220>
<223> 38kD

```

```

<400> 8
Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
  1             5             10             15

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
      20             25             30

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
      35             40             45

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
      50             55             60

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
      65             70             75             80

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
      85             90             95

Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
      100            105            110

Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
      115            120            125

Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
      130            135            140

Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
      145            150            155            160

Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
      165            170            175

Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
      180            185            190

Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
      195            200            205

```

Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

<210> 9
 <211> 327
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb11 (Tb38-1)

<400> 9
 cggcagcaga gaccgatgcc gctaccctcg cgcaggagge aggtaatctc gagcggatct 60
 ccggcgacct gaaaaccag atcgaccagg tggagtcgac ggcaggttcg ttgcagggcc 120
 agtggcgagg cgcgcgagg acggccgccc aggcgcgggt ggtgcgcttc caagaagcag 180
 ccaataagca gaagcaggaa ctcgacgaga tctcgacgaa tattcgctcag gccggcgctcc 240
 aatactcgag ggccgacgag gaggcagcag aggcgctgtc ctcgcaaagt ggcttctgac 300
 ccgctaatac gaaaagaaac ggagcaa 327

<210> 10
 <211> 95
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb11 (Tb38-1)

```

<400> 10
Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
 1           5           10           15
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
      20           25           30
Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
      35           40           45
Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
      50           55           60
Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
      65           70           75           80
Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
      85           90           95

```

```

<210> 11
<211> 702
<212> DNA
<213> Mycobacterium tuberculosis

```

```

<220>
<223> TbH4

```

```

<220>
<221> modified_base
<222> (1)..(702)
<223> n = g, a, c or t

```

```

<400> 11
cggcacgagg atcgggtaccc cgcggcatcg gcagctgccg attcgccggg tttccccacc 60
cgaggaaagc cgctaccaga tggcgctgcc gaagtagggc gatccgttcg cgatgccggc 120
atgaacgggc ggcatacaat tagtgacgga acctttcagt ttagcgacga taatggctat 180
agcactaagg aggatgatcc gatatgacgc agtcgcagac cgtgacgggtg gatcagcaag 240
agattttgaa cagggccaac gaggtggagg ccccgatggc ggaccaccg actgatgtcc 300
ccatcacacc gtgcgaactc acgnggnta aaaacgccgc ccaacagntg gtnttgctcg 360
ccgacaacat gcgggaatac ctggcgggccg gtgccaaaga gcggcagcgt ctggcgacct 420
cgctgcgcaa cgcggccaag gngtatggcg aggttgatga ggaggctgcg accgcgctgg 480
acaacgacgg cgaaggaact gtgcaggcag aatcggcccg ggccgtcgga ggggacagtt 540
cggccgaact aaccgatacg ccgaggggtg ccacggcccg tgaacccaac ttcattggatc 600
tcaaagaagc ggcaaggaag ctcgaaacgg gcgaccaagg cgcacgctc gcgcactgng 660
gggatgggtg gaacacttnc accctgacgc tgcaaggcga cg 702

```

```

<210> 12
<211> 286
<212> PRT
<213> Mycobacterium tuberculosis

```

```

<220>
<223> TbH4

```

```

<220>
<221> MOD_RES
<222> (1)..(286)
<223> Xaa = any amino acid

```

<400> 12

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
1 5 10 15

Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
20 25 30

His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
35 40 45

Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
50 55 60

Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
65 70 75 80

Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
85 90 95

Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
100 105 110

Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
115 120 125

Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
130 135 140

Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
145 150 155 160

Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
165 170 175

Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
180 185 190

Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
195 200 205

Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
210 215 220

Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
225 230 235 240

Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
245 250 255

Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
260 265 270

Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
275 280 285

<210> 13

<211> 1200

<212> DNA

<213> Mycobacterium tuberculosis

```

<400> 13
caggcatgag cagagcgttc atcatcgatc caacgatcag tgccattgac ggcttgtacg 60
accttctggg gattggaata cccaaccaag ggggtatcct ttactcctca ctagagtact 120
tcgaaaaaag cctggaggag ctggcagcag cgtttccggg tgatggctgg ttaggttcgg 180
ccgcggacaa atacgccggc aaaaaccgca accacgtgaa tttttccag gaactggcag 240
acctcgatcg tcagctcatc agcctgatcc acgaccaggc caacgcggtc cagacgacct 300
gcgacatcct ggagggcgcc aagaaaggtc tcgagttcgt gcgcccggtg gctgtggacc 360
tgacctacat cccggtcgtc gggcacgccc tatcgccgcg cttccaggcg ccgttttgcg 420
cgggcgcgat ggccgtagtg ggcggcgcgc ttgcctactt ggtcgtgaaa acgctgatca 480
acgcgactca actcctcaaa ttgcttgcca aattggcgga gttggtcgcg gccgccattg 540
cggacatcat ttcggatgtg gcggacatca tcaagggcac cctcggagaa gtgtgggagt 600
tcatcacaaa cgcgctcaac ggctgaaag agctttggga caagctcacg ggggtgggtga 660
ccggactgtt ctctcgaggg tggtcgaacc tggagtcctt ctttgcgggc gtccccggct 720
tgaccggcgc gaccagcggc ttgtcgcaag tgactggcct gttcgggtgcg gccggtctgt 780
ccgcacgcgc gggcttggct cacgcggata gcctggcgag ctcagccagc ttgcccgccc 840
tggccggcat tggggcgagg tccggttttg ggggcttgcc gagcctggct caggtccatg 900
ccgcctcaac tcggcaggcg ctacggcccc gagctgatgg cccggtcggc gccgctgccg 960
agcaggctcg cgggcagtcg cagctggtct ccgcgcaggg ttccaaggt atgggcggac 1020
ccgtaggcat gggcggcatg caccctctt cggggcgctc gaaagggacg acgacgaaga 1080
agtactcgga aggcgcggcg gcgggcactg aagacgccga gcgcgcgcca gtcgaagctg 1140
acgcgggcgg tgggcaaaaag gtgctggtac gaaacgtcgt ctaacggcat ggcgagccaa 1200

```

```

<210> 14
<211> 392
<212> PRT
<213> Mycobacterium tuberculosis

```

```

<220>
<223> HTCC#1 (Mtb40)

```

```

<400> 14
Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
  1             5             10             15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
      20             25             30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
      35             40             45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
      50             55             60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
      65             70             75             80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
      85             90             95

Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
      100            105            110

Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
      115            120            125

Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
      130            135            140

Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
      145            150            155            160

```


Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
 180 185 190
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 370 375 380
 Lys Val Leu Val Arg Asn Val Val
 385 390

<210> 15

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 (1-232)

<220>

<221> CDS

<222> (1)..(720)

<400> 15
atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat cca 48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
1 5 10 15
acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata 96
Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
20 25 30
ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa 144
Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
35 40 45
gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt 192
Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
50 55 60
tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt 240
Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
65 70 75 80
ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac 288
Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
85 90 95
gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc 336
Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
100 105 110
aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac 384
Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
115 120 125
atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg ttt 432
Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
130 135 140
tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt gcc tac ttg gtc 480
Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val
145 150 155 160
gtg aaa acg ctg atc aac gcg act caa ctc ctc aaa ttg ctt gcc aaa 528
Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys
165 170 175
ttg gcg gag ttg gtc gcg gcc gcc att gcg gac atc att tcg gat gtg 576
Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
180 185 190
gcg gac atc atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc aca 624
Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr
195 200 205
aac gcg ctc aac ggc ctg aaa gag ctt tgg gac aag ctc acg ggg tgg 672
Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp
210 215 220

gtg acc gga ctg ttc tct cga ggg tgg tcg aac ctg gag tcc ttc taa 720
 Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe
 225 230 235 240

gaattc 726

<210> 16
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 (1-232)

<400> 16
 Met His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
 1 5 10 15
 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
 20 25 30
 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
 35 40 45
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
 50 55 60
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
 65 70 75 80
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
 85 90 95
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
 100 105 110
 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
 115 120 125
 Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
 130 135 140
 Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val
 145 150 155 160
 Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys
 165 170 175
 Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
 180 185 190
 Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr
 195 200 205
 Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp
 210 215 220
 Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe
 225 230 235

<210> 17
 <211> 661
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1
 (184-392)

<220>
 <221> CDS
 <222> (1)..(651)

```

<400> 17
atg cat cac cat cac cat cac gat gtg gcg gac atc atc aag ggc atc   48
Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Ile
   1             5             10             15

ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa   96
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
      20             25             30

gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga  144
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
      35             40             45

ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc  192
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
      50             55             60

ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc  240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
      65             70             75             80

ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc  288
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
      85             90             95

tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt  336
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
      100            105            110

ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg cag  384
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
      115            120            125

gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag  432
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
      130            135            140

gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg  480
Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
      145            150            155            160

ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg  528
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
      165            170            175

aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act  576
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
      180            185            190

```

gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa 624
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 195 200 205

aag gtg ctg gta cga aac gtc gtc taa cggcgaattc 661
 Lys Val Leu Val Arg Asn Val Val
 210 215

<210> 18
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1
 (184-392)

<400> 18
 Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Ile
 1 5 10 15

Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 20 25 30

Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 35 40 45

Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 50 55 60

Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 65 70 75 80

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 85 90 95

Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 100 105 110

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 115 120 125

Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 130 135 140

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 145 150 155 160

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 165 170 175

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 180 185 190

Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 195 200 205

Lys Val Leu Val Arg Asn Val Val
 210 215

<210> 19
 <211> 411
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 (1-129)

<220>
 <221> CDS
 <222> (1)..(411)

```

<400> 19
atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat cca 48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
  1             5             10             15

acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata 96
Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
      20             25             30

ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa 144
Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
      35             40             45

gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt 192
Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
      50             55             60

tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt 240
Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
      65             70             75             80

ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac 288
Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
      85             90             95

gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc 336
Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
      100            105            110

aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac 384
Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
      115            120            125

atc ccg gtc gtc ggg cac gcc cta tag 411
Ile Pro Val Val Gly His Ala Leu
      130            135

```

<210> 20
 <211> 136
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 (1-129)

```

<400> 20
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
  1             5             10             15

```

Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
 20 25 30
 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
 35 40 45
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
 50 55 60
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
 65 70 75 80
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
 85 90 95
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
 100 105 110
 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
 115 120 125
 Ile Pro Val Val Gly His Ala Leu
 130 135

<210> 21
 <211> 1225
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 (TM-1)

<220>
 <221> CDS
 <222> (4)..(1215)

<400> 21
 cat atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat 48
 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp
 1 5 10 15
 cca acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga 96
 Pro Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly
 20 25 30
 ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa 144
 Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu
 35 40 45
 aaa gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta 192
 Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu
 50 55 60
 ggt tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat 240
 Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn
 65 70 75
 ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc 288
 Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile
 80 85 90 95

cac gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc	336
His Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly	
100 105 110	
gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc	384
Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr	
115 120 125	
tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg	432
Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro	
130 135 140	
ttt tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt aag ctt gcc	480
Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Ala	
145 150 155	
tac ttg gtc gtg aaa acg ctg atc aac gcg aag ctt act caa ctc ctc	528
Tyr Leu Val Val Lys Thr Leu Ile Asn Ala Lys Leu Thr Gln Leu Leu	
160 165 170 175	
aaa ttg ctt gcc aaa ttg gcg gag ttg gtc gcg gcc gcc att gcg gac	576
Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp	
180 185 190	
atc att tcg gat gtg gcg gac atc atc aag ggc atc ctc gga gaa gtg	624
Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val	
195 200 205	
tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa gag ctt tgg gac	672
Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp	
210 215 220	
aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga ggg tgg tcg aac	720
Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn	
225 230 235	
ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc ggc gcg acc agc	768
Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser	
240 245 250 255	
ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca	816
Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala	
260 265 270	
tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc tca gcc agc ttg	864
Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu	
275 280 285	
ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt ggg ggc ttg ccg	912
Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro	
290 295 300	
agc ctg gct cag gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc	960
Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro	
305 310 315	
cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag gtc ggc ggg cag	1008
Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln	
320 325 330 335	

tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta 1056
 Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val
 340 345 350
 ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg 1104
 Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr
 355 360 365
 acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag 1152
 Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu
 370 375 380
 cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta 1200
 Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val
 385 390 395
 cga aac gtc gtc taa cggcgaattc 1225
 Arg Asn Val Val
 400

<210> 22
 <211> 403
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 (TM-1)

<400> 22
 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
 1 5 10 15
 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
 20 25 30
 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
 35 40 45
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
 50 55 60
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
 65 70 75 80
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
 85 90 95
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
 100 105 110
 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
 115 120 125
 Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
 130 135 140
 Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Ala Tyr
 145 150 155 160

Leu Val Val Lys Thr Leu Ile Asn Ala Lys Leu Thr Gln Leu Leu Lys
 165 170 175
 Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile
 180 185 190
 Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp
 195 200 205
 Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys
 210 215 220
 Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu
 225 230 235 240
 Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly
 245 250 255
 Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser
 260 265 270
 Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro
 275 280 285
 Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser
 290 295 300
 Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg
 305 310 315 320
 Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser
 325 330 335
 Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
 340 345 350
 Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr
 355 360 365
 Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg
 370 375 380
 Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg
 385 390 395 400
 Asn Val Val

<210> 23

<211> 1225

<212> DNA.

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 (TM-2)

<220>

<221> CDS

<222> (4)..(1215)

<400> 23

cat atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat	48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp	
1 5 10 15	
cca acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga	96
Pro Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly	
20 25 30	
ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa	144
Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu	
35 40 45	
aaa gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta	192
Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu	
50 55 60	
ggt tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat	240
Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn	
65 70 75	
ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc	288
Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile	
80 85 90 95	
cac gac cag gcc aac gcg gtc cag acg acc cgc gac aag ctt atc ctg	336
His Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Lys Leu Ile Leu	
100 105 110	
gag ggc gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac	384
Glu Gly Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp	
115 120 125	
ctg acc tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag	432
Leu Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln	
130 135 140	
gcg ccg ttt tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt gcc	480
Ala Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala	
145 150 155	
tac ttg gtc gtg aaa acg ctg atc aac gcg act caa ctc ctc aaa ttg	528
Tyr Leu Val Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu	
160 165 170 175	
ctt gcc aaa ttg gcg gag ttg gtc gcg gcc gcc att gcg gac atc att	576
Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ile Ala Asp Ile Ile	
180 185 190	
tcg gat gtg gcg gac atc atc aag ggc atc ctc gga gaa gtg tgg gag	624
Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu	
195 200 205	
ttc atc aca aac gcg aag ctt ctc aac ggc ctg aaa gag ctt tgg gac	672
Phe Ile Thr Asn Ala Lys Leu Leu Asn Gly Leu Lys Glu Leu Trp Asp	
210 215 220	
aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga ggg tgg tcg aac	720
Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn	
225 230 235	

ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc ggc gcg acc agc	768
Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser	
240 245 250 255	
ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca	816
Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala	
260 265 270	
tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc tca gcc agc ttg	864
Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu	
275 280 285	
ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt ggg ggc ttg ccg	912
Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro	
290 295 300	
agc ctg gct cag gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc	960
Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro	
305 310 315	
cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag gtc ggc ggg cag	1008
Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln	
320 325 330 335	
tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta	1056
Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val	
340 345 350	
ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg	1104
Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr	
355 360 365	
acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag	1152
Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu	
370 375 380	
cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta	1200
Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val	
385 390 395	
cga aac gtc gtc taa cggcgaattc	1225
Arg Asn Val Val	
400	

<210> 24

<211> 403

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 (TM-2)

<400> 24

Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro	
1 5 10 15	
Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile	
20 25 30	

Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
 35 40 45
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
 50 55 60
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
 65 70 75 80
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
 85 90 95
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Lys Leu Ile Leu Glu
 100 105 110
 Gly Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu
 115 120 125
 Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala
 130 135 140
 Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr
 145 150 155 160
 Leu Val Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu
 165 170 175
 Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser
 180 185 190
 Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe
 195 200 205
 Ile Thr Asn Ala Lys Leu Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys
 210 215 220
 Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu
 225 230 235 240
 Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly
 245 250 255
 Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser
 260 265 270
 Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro
 275 280 285
 Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser
 290 295 300
 Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg
 305 310 315 320
 Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser
 325 330 335
 Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
 340 345 350

Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr
 355 360 365

Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg
 370 375 380

Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg
 385 390 395 400

Asn Val Val

<210> 25

<211> 3058

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> TbH9 (Mtb39A)

<400> 25

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tgtggctagc aatgccgctg cggcgccccc gacgactggg gtggtgcccc ccgctgccga 180
tgagggtgtcg gcgctgactg cggcgccactt cgccgcacat gcggcgatgt atcagtccgt 240
gagcgctcgg gctgctgcga ttcattgacca gttcgtggcc acccttgcca gcagcgccag 300
ctcgtatgct gccactgaag tcgccaatgc ggcgccggcc agctaagcca ggaacagtcg 360
gcacgagaaa ccacgagaaa tagggacacg taatggtgga tttcggggcg ttaccaccgg 420
agatcaactc cgcgaggatg tacgcccggc cgggttcggc ctcgctggtg gccgcccgtc 480
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cctcgccgta tgtggcggtg atgagcgtca ccgccccgca ggccgagctg accgcccggc 660
aggtccgggt tgcctgcggc gcctacgaga cggcgatagg gctgacgggt cccccgccgg 720
tgatcgccga gaaccgtgct gaactgatga ttctgatagc gaccaacctc ttggggcaaa 780
acaccccggc gatcgcggtc aacgaggccg aatacgccga gatgtgggcc caagacgccg 840
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ttccgcggcc ggctatgaca acagtcaatg tgcattgaca gttacaggta ttaggtccag 1680
gttcaacaag gagacaggca acatggcctc acgttttatg acggatccgc acgcgatgcg 1740
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gtgggcgtcc gcgcaaaaca tttccggtgc gggctggagt ggcattggcc aggcgacctc 1860
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gccggcaaca acatggcgca aaccgacagc gccgtcggct ccagctgggc ctgacaccag 2340
gccaaggcca gggacgtggt gtacgagtga agttcctcgc gtgatccttc ggggtggcag 2400

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ctaagtggtc agtgctgggg tgttggtggt ttgctgcttg gcggggttctt cgggtgctggt 2460
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```

<210> 26

<211> 391

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> TbH9 (Mtb39A)

<400> 26

```

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
  1              5              10              15

```

```

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
      20              25              30

```

```

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
      35              40              45

```

```

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
      50              55              60

```

```

Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
      65              70              75              80

```

```

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
      85              90              95

```

```

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
      100              105              110

```

```

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
      115              120              125

```

```

Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
      130              135              140

```

```

Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
      145              150              155              160

```

```

Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
      165              170              175

```

```

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
      180              185              190

```

```

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
      195              200              205

```

Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380
 Pro His Ser Pro Ala Ala Gly
 385 390

<210> 27
 <211> 447
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> TbRa12

<400> 27
 cggtatgaac acggccgcgt ccgataactt ccagctgtcc caggggtgggc agggattcgc 60
 cattccgatc gggcaggcga tggcgatcgc gggccagatc cgatcgggtg gggggtcacc 120
 caccgttcac atcgggccta ccgccttccct cggcttgggt gttgtcgaca acaacggcaa 180
 cggcgacga gtccaacgcg tggtcgggag cgctccggcg gcaagtctcg gcatctccac 240
 cggcgacgtg atcaccgcgg tcgacggcgc tccgatcaac tcggccaccg cgatggcgga 300
 cgcgcttaac gggcatcatc ccggtgacgt catctcgggtg aactggcaaa ccaagtcggg 360
 cggcacgcgt acagggaacg tgacattggc cgaggggaccc ccggcctgat ttcgtcgygg 420
 ataccacccg ccggccggcc aattgga 447

<210> 28
 <211> 132
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> TbRa12

<400> 28
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20 25 30
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
 100 105 110
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 115 120 125
 Gly Pro Pro Ala
 130

<210> 29
 <211> 1872
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> TbRa35 (Mtb32A)

<220>
 <221> modified_base
 <222> (1)..(1872)
 <223> n = g, a, c or t

<400> 29
 gactacgttg gtgtagaaaa atcctgcccgc ccggaccctt aaggctggga caatttctga 60
 tagctacccc gacacaggag gttacgggat gagcaattcg cgccgccgct cactcagggtg 120
 gtcattggttg ctgagcgtgc tggctgccgt cgggctgggc ctggccacgg cgccggccca 180
 ggcggccccc ccggccttgt cgcaggaccg gttcgccgac ttccccgcgc tgccctcga 240
 cccgtccgcg atggtcgccc aagtggcgcc acaggtggtc aacatcaaca ccaaactggg 300
 ctacaacaac gccgtgggcg ccgggaccgg catcgatcat gatcccaacg gtgtcgtgct 360
 gaccaacaac cacgtgatcg cgggcccacc cgacatcaat gcgttcagcg tgggtcccg 420
 ccaaacctac ggcgtcgatg tggctgggta tgaccgcacc caggatgtcg cgggtgctgca 480
 gctgcgcggt gccggtggcc tgccgtcggc ggcgatcggg ggccgctcg cgggttggtga 540
 gcccgctcgc gcgatgggca acagcgttgg gcagggcgga acgcccctg cgggtgcctgg 600
 cagggtggtc gcgctcggcc aaaccgtgca ggcgtcggat tcgctgaccg gtgccgaaga 660
 gacattgaac gggttgatcc agttcgatgc cgcaatccag cccggtgatt cgggcgggccc 720
 cgctcgtcaac ggcctaggac aggtggtcgg tatgaacacg gccgcgtccg ataacttcca 780
 gctgtcccag ggtgggcagg gattcgccat tccgatcggg caggcgatgg cgatcgccgg 840
 ccaaattccga tcgggtgggg ggtcaccac cgttcatatc gggcctaccg ccttcctcgg 900

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cttgggtgtt gtcgacaaca acggcaacgg cgcacgagtc caacgcgtgg tcggaagcgc 960
tccggcggca agtctcggca tctccaccgg cgacgtgata accgcggtcg acggcgctcc 1020
gatcaactcg gccaccgcga tggcggacgc gcttaacggg catcatcccc gtgacgtcat 1080
ctcggtgaaac tggcaaacca agtcgggagg cagcgtatac gggaacgtga cattggccga 1140
gggacccccg gcctgatttg tcgcggtata caccgcggcg ccggccaatt ggattggcgc 1200
cagccgtgat tgccgcgtga gccccgagt tccgtctccc gtgcgcgtgg cattgtggaa 1260
gcaatgaacg aggcagaaca cagcgttgag caccctcccc tgcagggcag ttacgtcgaa 1320
ggcgggtgtg tcgagcatcc ggatgccaag gacttcggca gcgccgccgc cctgccccgc 1380
gatccgacct ggtttaagca cgccgtcttc tacgaggtgc tggtcggggc gttcttcgac 1440
gccagcgagg acggttccgn cgatctgcgt ggactcatcg atcgctcga ctacctgcag 1500
tggcttgcca tcgactgcat ctggtgccgc cgttcctacg actcaccgct gcgcgacggc 1560
ggttacgaca ttcgcgactt ctacaaggtg ctgcccgaat tcggcaccgt cgacgatttc 1620
gtcgccctgg tcgacaccgc tcaccggcga ggtatccgca tcatcaccga cctggtgatg 1680
aatcacacct cggagtcgca cccctggtt caggagtccc gccgcgaccc agacggaccg 1740
tacggtgact attacgtgtg gagcgacacc agcgagcgct acaccgacgc ccggatcatc 1800
ttcgtcgaca ccgaagagtc gaactggtca ttcgatcctg tccgccgaca gttntactg 1860
gcaccgattc tt                                     1872

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<210> 30
<211> 355
<212> PRT
<213> Mycobacterium tuberculosis

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<220>
<223> TbRa35 (Mtb32A)

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<400> 30
Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
 1             5             10            15
Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
      20             25             30
Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
      35             40             45
Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
      50             55             60
Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
      65             70             75             80
Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
      85             90             95
Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
      100            105            110
Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
      115            120            125
Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
      130            135            140
Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
      145            150            155            160
Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
      165            170            175

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Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
 355

<210> 31
 <211> 1441
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> MTCC#2 (Mtb41)

<400> 31
 gaggttgctg gcaatggatt tcgggctttt acctccggaa gtgaattcaa gccgaatgta 60
 ttccggtccg gggccggagt cgatgctagc cgccgcggcc gcctgggacg gtgtggccgc 120
 ggagttgact tccgccgcgg tctcgtagtg atcgggtggtg tcgacgctga tcgttgagcc 180
 gtggatgggg ccggcgggcg ccgcgatggc ggccgcggca acgccgtatg tggggtggct 240
 ggccgccacg gcggcgctgg cgaaggagac ggccacacag gcgagggcag cggcggaagc 300
 gtttgggacg gcgttcgcga tgacgggtgcc accatccctc gtcgcggcca accgcagccg 360
 gttgatgtcg ctggtcgcgg cgaacattct ggggcaaaac agtgcggcga tcgcggctac 420
 ccaggccgag tatgccgaaa tgtgggcccc agacgctgcc gtgatgtaca gctatgaggg 480
 ggcattctcg gccgcgtcgg cgttgccgcc gttcactcca cccgtgcaag gcaccggccc 540
 ggccgggccc gcggccgcag ccgcggcgac ccaagccgcc ggtgcgggcg ccgttgcgga 600
 tgcacaggcg acactggccc agctgcccc ggggatcctg agcgacattc tgtccgcatt 660
 ggccgccaac gctgatccgc tgacatcggg actgttgggg atcgcgctga ccctcaaccc 720
 gcaagtcgga tccgctcagc cgatagtgat cccaccccc ataggggaat tggacgtgat 780
 cgcgctctac attgcatcca tcgcgaccgg cagcattgcg ctgcgcatca cgaacacggc 840
 cagaccctgg cacatcggcc tatacgggaa cgccggcggg ctgggaccga cgcagggcca 900

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tccactgagt tccggcgaccg acgagccgga gccgcactgg gggcccttcg ggggcgcggc 960
gccggtgtcc gcggggcgtcg gccacgcagc attagtcgga gcgttgtcg tgcgcacag 1020
ctggaccacg gccgccccgg agatccagct cgccgttcag gcaacaccca ccttcagctc 1080
cagcgccggc gccgaccga cggccctaaa cgggatgccg gcaggcctgc tcagcgggat 1140
ggctttggcg agcctggccg cacgcggcac gacgggcggg ggcggcaccc gtagcggcac 1200
cagcactgac ggccaagagg acggccgcaa acccccggtg gttgtgatta gagagcagcc 1260
gccgccccga aacccccgcg ggtaaaagtc cggcaaccgt tcgtcgccgc gcggaaaatg 1320
cctggtgagc gtggctatcc gacgggcccgt tcacaccgct tgtagtagcg tacggctatg 1380
gacgacggtg tctggattct cggcggctat cagagcgatt ttgctcgcaa cctcagcaaa 1440
g
1441

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<210> 32
<211> 423
<212> PRT
<213> Mycobacterium tuberculosis

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<220>
<223> MTTC#2 (Mtb41)

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```

<400> 32
Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
  1             5             10             15

Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp
          20             25             30

Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
          35             40             45

Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
          50             55             60

Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
          65             70             75             80

Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
          85             90             95

Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
          100            105            110

Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
          115            120            125

Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
          130            135            140

Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
          145            150            155            160

Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
          165            170            175

Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
          180            185            190

Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
          195            200            205

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Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
 210 215 220
 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
 225 230 235 240
 Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
 245 250 255
 Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
 260 265 270
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
 275 280 285
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
 290 295 300
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
 305 310 315 320
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
 325 330 335
 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
 340 345 350
 Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
 355 360 365
 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
 370 375 380
 Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
 405 410 415
 Pro Pro Gly Asn Pro Pro Arg
 420

<210> 33
 <211> 1742
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb9.9A (MTI-A)

<220>
 <221> modified_base
 <222> (1)..(1742)
 <223> n = g, a, c or t

<400> 33
 ccgctctctt tcaacgtcat aagttcgggtg ggccagtcgg ccgcgcggtgc atatggcacc 60
 aataacgcgt gtcccatgga taccgggacc gcacgacggt agagcggatc agcgcagccg 120
 gtgccgaaca ctaccgcgtc cacgctcagc cctgccgcgt tgcggaagat cgagcccagg 180
 ttctcatggt cgттаacgcc ttccaacact gcgacgggtgc gcgccccggc gaccacctga 240

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gcaacgctcg gctccggcac ccggcgcgcg gctgccaaca cccacgatt gagatggaag 300
ccgatcaccg gtgccatgac atcagccgac gctcgatagt acggcgcgcc gacaccggcc 360
agatcatcct tgagctcggc cagccggcgg tcggtgccga acagcgccag cggcgtgaac 420
cgtgaggcca gcatgcgctg caccaccagc acaccctcgg cgatcaccaa cgccttgccg 480
gtcggcagat cgggacnacn gtcgatgctg ttcaggtcac ggaaatcgtc gagccgtggg 540
tcgtcgggat cgcagacgtc ctgaacatcg agggcgtcgg ggtgctgggc acaacggcct 600
tcggtcacgg gctttcgtcg accagagcca gcatcagatc ggcgcgctg cgcaggatgt 660
cacgctcgct gcggttcagc gtcgcgagcc gctcagccag ccactcttgc agagagccgt 720
tgctgggatt aattgggaga ggaagacagc atgtcgttcg tgaccacaca gccggaagcc 780
ctggcagctg cggcgcgcaa cctacagggg attggcacga caatgaacgc ccagaacgcg 840
gcccgcgctg ctccaaccac cggagtagtg cccgcagccg ccgatgaagt atcagcgctg 900
accgcggctc agtttgctgc gcacgcgcag atgtaccaaa cggtcagcgc ccaggccgcg 960
gccattcacg aaatgttcgt gaacacgctg gtggccagtt ctggctcata cgcggccacc 1020
gaggcggcca acgcagccgc tggcggtcgc acgaacctgc tgaaggagag 1080
ggggaacatc cggagttctc gggtcagggg ttgcgccagc gccagccga ttcagntatc 1140
ggcgctcata acagcagacg atctaggcat tcagtactaa ggagacaggc aacatggcct 1200
cacgttttat gacggatccg catgcgatgc gggacatggc gggccgtttt gaggtgcacg 1260
cccagacggt ggaggacgag gctcgccgga tgtgggcgtc cgcgcaaaac atttccggtg 1320
cgggctggag tggcatggcc gaggcgacct cgctagacac catgacctag atgaatcagg 1380
cgtttcgcaa catcgtgaac atgctgcacg ggggtgcgtg cgggctggtt cgcgacgcca 1440
acaantacga acagcaagag caggcctccc agcagatcct gagcagntag cgccgaaagc 1500
cacagctgng tacgntttct cacattagga gaacaccaat atgacgatta attaccagtt 1560
cggggacgtc gacgctcatg gcgccatgat ccgcgctcag gcggcgtcgc ttgaggcgga 1620
gcatcaggcc atcgttcgtg atgtgttggc cgcgggtgac ttttggggcg gcgccggttc 1680
ggtggcttgc caggagttca ttaccaggtt gggccgtaac ttccagggtg tctacgagca 1740
gg

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<210> 34
<211> 94
<212> PRT
<213> Mycobacterium tuberculosis

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<220>
<223> Mtb9.9A (MTI-A)

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<400> 34
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1             5             10            15

Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
      20             25             30

Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
      35             40             45

Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
      50             55             60

Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
      65             70             75            80

Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
      85             90

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```

<210> 35
<211> 585
<212> DNA
<213> Mycobacterium tuberculosis

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<220>
 <223> Mtb9.8 (MSL)

<400> 35
 tggattccga tagcgggtttc ggccccctcga cgggcgacca cggcgcgag gcctccgaac 60
 gggggggccgg gacgctggga ttccgccgga ccgcaaccaa agaacgccgg gtccggggcgg 120
 tcgggctgac cgcactggcc ggtgatgagt tcggcaacgg cccccggatg ccgatgggtgc 180
 cggggacctg ggagcagggc agcaacgagc ccgaggcgcc cgacggatcg gggagagggg 240
 gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggaccctgtac 300
 gggtcgaaaag gagagatggt atgagccttt tggatgctca tatcccacag ttgggtggcct 360
 cccagtcggc gtttgccgcc aaggcggggc tgatgcggca cacgatcggg caggccgagc 420
 aggcggcgat gtcggctcag gcgtttcacc agggggagtc gtcggcgggc tttcaggccg 480
 cccatgcccg gtttgtggcg gcggccgcc aagtcaacac cttgttgat gtcgcgagc 540
 cgaatctggg tgaggccgcc ggtacctatg tggccgccga tgctg 585

<210> 36
 <211> 97
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb9.8 (MSL)

<400> 36
 Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1 5 10 15
 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20 25 30
 Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35 40 45
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

<210> 37
 <211> 500
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb8.4 (DPV)

<400> 37
 cgtggcaatg tcgttgaccg tcggggccgg ggtcgccctc gcagatcccg tggacgcggg 60
 cattaacacc acctgcaatt acgggcaggt agtagctgcg ctcaacgcga cggatccggg 120
 ggctgccgca cagttcaacg cctcaccggg ggcgcagtcg tatttgcgca atttcctcgc 180
 cgcaccgcc cctcagcgcg ctgccatggc cgcgcaattg caagctgtgc cggggggcggc 240
 acagtacatc ggccttgctg agtcggttgc cggctcctgc aacaactatt aagcccatgc 300
 gggcccatc cgcgcacccg gcatcgctgc cggggctagg ccagattgcc ccgctcctca 360

acggggcgcga tcccgcgacc cggcatcgtc gccgggggcta ggccagattg ccccgtcct 420
 caacggggcg catctcgtgc cgaattcctg cagcccgggg gatccactag ttctagagcg 480
 gccgccaccg cggaggagct 500

<210> 38
 <211> 96
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb8.4 (DPV)

<400> 38
 Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
 1 5 10 15
 Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
 20 25 30
 Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
 35 40 45
 Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
 50 55 60
 Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
 65 70 75 80
 Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
 85 90 95

<210> 39
 <211> 999
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> DPEP

<400> 39
 atgcatcacc atcaccatca catgcatcag gtggacccca acttgacacg tcgcaaggga 60
 cgattggcgg cactggctat cgcggcgatg gccagcgcca gcctgggtgac cgttgcggtg 120
 cccgcgaccg ccaacgccga tccggagcca gcgcccccgg taccacacaac ggccgcctcg 180
 ccgcccgtcga ccgctgcagc gccaccgcga ccggcgacac ctgttgcccc cccaccaccg 240
 gccgccgcca acacgccgaa tgcccagccg ggcgatccca acgcagcacc tccgccggcc 300
 gaccgaacg caccgccgcc acctgtcatt gccccaaacg caccacaacc tgtccggatc 360
 gacaaccggg ttggaggatt cagcttcgcg ctgcctgctg gctgggtgga gtctgacgcc 420
 gccacttcg actacggttc agcactcctc agcaaaacca ccgggggaccc gccatttccc 480
 ggacagccgc cgccggtggc caatgacacc cgtatcgtgc tcggccgggt agacaaaaag 540
 ctttacgccg gcgcgaagc caccgactcc aaggccgcgg cccggttggg ctcggaacatg 600
 ggtgagttct atatgcccta cccgggcacc cggatcaacc aggaaccgt ctgcctcgac 660
 gccaacgggg tgtctggaag cgcgtcgtat tacgaagtca agttcagcga tccgagtaag 720
 ccgaacggcc agatctggac gggcgtaatc ggctcgcccc cggcgaaacg accggacgcc 780
 gggccccctc agcgtggtt tgtggtatgg ctcgggaccg ccaacaaccc ggtggacaag 840
 ggcgcggcca aggcgtggc cgaatcgatc cggcctttgg tcgccccgcc gccggcgccg 900
 gcaccggctc ctgcagagcc cgctccggcg ccggcgccgg ccgggggaagt cgctcctacc 960
 ccgacgacac cgacaccgca gcggacctta ccggcctga 999

<210> 40
 <211> 332
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> DPEP

<400> 40

Met	His	His	His	His	His	His	Met	His	Gln	Val	Asp	Pro	Asn	Leu	Thr
1				5					10					15	
Arg	Arg	Lys	Gly	Arg	Leu	Ala	Ala	Leu	Ala	Ile	Ala	Ala	Met	Ala	Ser
			20					25					30		
Ala	Ser	Leu	Val	Thr	Val	Ala	Val	Pro	Ala	Thr	Ala	Asn	Ala	Asp	Pro
		35					40					45			
Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro	Ser	Thr
	50					55					60				
Ala	Ala	Ala	Pro	Pro	Ala	Pro	Ala	Thr	Pro	Val	Ala	Pro	Pro	Pro	Pro
65					70					75					80
Ala	Ala	Ala	Asn	Thr	Pro	Asn	Ala	Gln	Pro	Gly	Asp	Pro	Asn	Ala	Ala
			85					90						95	
Pro	Pro	Pro	Ala	Asp	Pro	Asn	Ala	Pro	Pro	Pro	Pro	Val	Ile	Ala	Pro
			100					105					110		
Asn	Ala	Pro	Gln	Pro	Val	Arg	Ile	Asp	Asn	Pro	Val	Gly	Gly	Phe	Ser
		115					120					125			
Phe	Ala	Leu	Pro	Ala	Gly	Trp	Val	Glu	Ser	Asp	Ala	Ala	His	Phe	Asp
	130					135					140				
Tyr	Gly	Ser	Ala	Leu	Leu	Ser	Lys	Thr	Thr	Gly	Asp	Pro	Pro	Phe	Pro
145					150					155					160
Gly	Gln	Pro	Pro	Pro	Val	Ala	Asn	Asp	Thr	Arg	Ile	Val	Leu	Gly	Arg
				165					170					175	
Leu	Asp	Gln	Lys	Leu	Tyr	Ala	Ser	Ala	Glu	Ala	Thr	Asp	Ser	Lys	Ala
			180					185					190		
Ala	Ala	Arg	Leu	Gly	Ser	Asp	Met	Gly	Glu	Phe	Tyr	Met	Pro	Tyr	Pro
		195					200					205			
Gly	Thr	Arg	Ile	Asn	Gln	Glu	Thr	Val	Ser	Leu	Asp	Ala	Asn	Gly	Val
	210					215					220				
Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys	Phe	Ser	Asp	Pro	Ser	Lys
225					230					235					240
Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile	Gly	Ser	Pro	Ala	Ala	Asn
				245					250					255	
Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp	Phe	Val	Val	Trp	Leu	Gly
			260					265					270		

Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
 275 280 285

Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
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Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
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Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
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<210> 41

<400> 41

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<210> 42

<400> 42

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<210> 43

<211> 339

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> DPPD

<400> 43

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<211> 112

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> DPPD

<400> 44

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Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
 35 40 45

Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
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Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
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Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
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Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
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<210> 45
 <211> 154
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> ESAT-6

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 aatgtcacgt ccattcattc cctccttgac gaggggaagc agtccctgac caagctcgca 120
 gcggcctggg gcggtagcgg ttcggaagcg tacc 154

<210> 46
 <211> 51
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> ESAT-6

<400> 46
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 Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
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 Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
 35 40 45
 Glu Ala Tyr
 50

<210> 47
 <211> 2310
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb82

<400> 47
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 aacgttcggg ccccggcacc caaccggcgg acgcccagac cgcgacgtcc gcgacgggtc 120
 gacccttgag caccagggcg gtgttcgcc ccgatttcgg cgatgaggac aacttcccc 180

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<210> 48
 <211> 750
 <212> PRT
 <213> *Mycobacterium tuberculosis*

<220>
 <223> Mtb82

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 35 40 45
 Pro Thr Leu Gly Pro Asp Thr Glu Pro Gln Asp Arg Met Ala Thr Thr
 50 55 60
 Ser Arg Val Arg Pro Pro Val Arg Arg Leu Gly Gly Gly Leu Val Glu
 65 70 75 80

Ile Pro Arg Ala Pro Asp Ile Asp Pro Leu Glu Ala Leu Met Thr Asn
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 Pro Val Val Pro Glu Ser Lys Arg Phe Cys Trp Asn Cys Gly Arg Pro
 100 105 110
 Val Gly Arg Ser Asp Ser Glu Thr Lys Gly Ala Ser Glu Gly Trp Cys
 115 120 125
 Pro Tyr Cys Gly Ser Pro Tyr Ser Phe Leu Pro Gln Leu Asn Pro Gly
 130 135 140
 Asp Ile Val Ala Gly Gln Tyr Glu Val Lys Gly Cys Ile Ala His Gly
 145 150 155 160
 Gly Leu Gly Trp Ile Tyr Leu Ala Leu Asp Arg Asn Val Asn Gly Arg
 165 170 175
 Pro Val Val Leu Lys Gly Leu Val His Ser Gly Asp Ala Glu Ala Gln
 180 185 190
 Ala Met Ala Met Ala Glu Arg Gln Phe Leu Ala Glu Val Val His Pro
 195 200 205
 Ser Ile Val Gln Ile Phe Asn Phe Val Glu His Thr Asp Arg His Gly
 210 215 220
 Asp Pro Val Gly Tyr Ile Val Met Glu Tyr Val Gly Gly Gln Ser Leu
 225 230 235 240
 Lys Arg Ser Lys Gly Gln Lys Leu Pro Val Ala Glu Ala Ile Ala Tyr
 245 250 255
 Leu Leu Glu Ile Leu Pro Ala Leu Ser Tyr Leu His Ser Ile Gly Leu
 260 265 270
 Val Tyr Asn Asp Leu Lys Pro Glu Asn Ile Met Leu Thr Glu Glu Gln
 275 280 285
 Leu Lys Leu Ile Asp Leu Gly Ala Val Ser Arg Ile Asn Ser Phe Gly
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 305 310 315 320
 Gly Pro Thr Val Ala Thr Asp Ile Tyr Thr Val Gly Arg Thr Leu Ala
 325 330 335
 Ala Leu Thr Leu Asp Leu Pro Thr Arg Asn Gly Arg Tyr Val Asp Gly
 340 345 350
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 Leu Leu Arg Arg Ala Ile Asp Pro Asp Pro Arg Gln Arg Phe Thr Thr
 370 375 380
 Ala Glu Glu Met Ser Ala Gln Leu Thr Gly Val Leu Arg Glu Val Val
 385 390 395 400

Ala Gln Asp Thr Gly Val Pro Arg Pro Gly Leu Ser Thr Ile Phe Ser
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 Pro Ser Arg Ser Thr Phe Gly Val Asp Leu Leu Val Ala His Thr Asp
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 Val Tyr Leu Asp Gly Gln Val His Ala Glu Lys Leu Thr Ala Asn Glu
 435 440 445
 Ile Val Thr Ala Leu Ser Val Pro Leu Val Asp Pro Thr Asp Val Ala
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 Ala Ser Val Leu Gln Ala Thr Val Leu Ser Gln Pro Val Gln Thr Leu
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 485 490 495
 Asp Phe Ser Glu Ser Val Glu Leu Pro Leu Met Glu Val Arg Ala Leu
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 Leu Asp Leu Gly Asp Val Ala Lys Ala Thr Arg Lys Leu Asp Asp Leu
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 530 535 540
 Ala Glu Leu Leu Thr Gly Asp Tyr Asp Ser Ala Thr Lys His Phe Thr
 545 550 555 560
 Glu Val Leu Asp Thr Phe Pro Gly Glu Leu Ala Pro Lys Leu Ala Leu
 565 570 575
 Ala Ala Thr Ala Glu Leu Ala Gly Asn Thr Asp Glu His Lys Phe Tyr
 580 585 590
 Gln Thr Val Trp Ser Thr Asn Asp Gly Val Ile Ser Ala Ala Phe Gly
 595 600 605
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 645 650 655
 Thr Glu Glu Gln Ile Arg Asp Ala Ala Arg Arg Val Glu Ala Leu Pro
 660 665 670
 Pro Thr Glu Pro Arg Val Leu Gln Ile Arg Ala Leu Val Leu Gly Gly
 675 680 685
 Ala Leu Asp Trp Leu Lys Asp Asn Lys Ala Ser Thr Asn His Ile Leu
 690 695 700
 Gly Phe Pro Phe Thr Ser His Gly Leu Arg Leu Gly Val Glu Ala Ser
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725 730 735

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<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb59

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<210> 50
<211> 549
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb59

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 35 40 45
 Ser Val Met Thr Gln Glu Leu Leu Glu Phe Pro Gly Gly Ile Leu Gly
 50 55 60
 Val Ala Leu Asn Leu Asp Glu His Ser Val Gly Ala Val Ile Leu Gly
 65 70 75 80
 Asp Phe Glu Asn Ile Glu Glu Gly Gln Gln Val Lys Arg Thr Gly Glu
 85 90 95
 Val Leu Ser Val Pro Val Gly Asp Gly Phe Leu Gly Arg Val Val Asn
 100 105 110
 Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr
 115 120 125
 Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val His Arg Gln Gly
 130 135 140
 Val Lys Glu Pro Leu Gln Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
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 Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
 165 170 175
 Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Arg Gln Asn
 180 185 190
 Trp Glu Ser Gly Asp Pro Lys Lys Gln Val Arg Cys Val Tyr Val Ala
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 Ile Gly Gln Lys Gly Thr Thr Ile Ala Ala Val Arg Arg Thr Leu Glu
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 Glu Gly Gly Ala Met Asp Tyr Thr Thr Ile Val Ala Ala Ala Ala Ser
 225 230 235 240
 Glu Ser Ala Gly Phe Lys Trp Leu Ala Pro Tyr Thr Gly Ser Ala Ile
 245 250 255
 Ala Gln His Trp Met Tyr Glu Gly Lys His Val Leu Ile Ile Phe Asp
 260 265 270
 Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu
 275 280 285
 Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu
 290 295 300
 His Ser Arg Leu Leu Glu Arg Cys Ala Lys Leu Ser Asp Asp Leu Gly
 305 310 315 320
 Gly Gly Ser Leu Thr Gly Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp
 325 330 335

Ile Ser Ala Tyr Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
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 Cys Phe Leu Glu Thr Asp Leu Phe Asn Gln Gly Val Arg Pro Ala Ile
 355 360 365
 Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Ile Lys
 370 375 380
 Ala Met Lys Glu Val Ala Gly Ser Leu Arg Leu Asp Leu Ser Gln Tyr
 385 390 395 400
 Arg Glu Leu Glu Ala Phe Ala Ala Phe Ala Ser Asp Leu Asp Ala Ala
 405 410 415
 Ser Lys Ala Gln Leu Glu Arg Gly Ala Arg Leu Val Glu Leu Leu Lys
 420 425 430
 Gln Pro Gln Ser Gln Pro Met Pro Val Glu Glu Gln Val Val Ser Ile
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 Phe Leu Gly Thr Gly Gly His Leu Asp Ser Val Pro Val Glu Asp Val
 450 455 460
 Arg Arg Phe Glu Thr Glu Leu Leu Asp His Met Arg Ala Ser Glu Glu
 465 470 475 480
 Glu Ile Leu Thr Glu Ile Arg Asp Ser Gln Lys Leu Thr Glu Glu Ala
 485 490 495
 Ala Asp Lys Leu Thr Glu Val Ile Lys Asn Phe Lys Lys Gly Phe Ala
 500 505 510
 Ala Thr Gly Gly Gly Ser Val Val Pro Asp Glu His Val Glu Ala Leu
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 Pro Lys Lys Lys Lys
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<210> 51

<211> 3523

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:TbF14 fusion protein

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agccaccccg	gggtcaccgc	gacgttctgt	gaggcgctgg	cggcgggtggg	ggtcaacatc	3360
gagctgatct	ccacctcgga	agatcagaga	tctcgtgtgt	gtgccgcgac	accgaactgg	3420
acaaggccgt	ggtcgcgctg	catgaagcgt	tcgggctcgg	cggcgacgag	gaggccacgg	3480
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<210> 52

<211> 1172

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:TbF14 fusion protein

<400> 52

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20 25 30
Pro Gly Thr Asp Ile Asp Pro Asp Ser Phe Trp Ala Gly Val Asp Lys
35 40 45
Val Val Ala Asp Leu Thr Pro Gln Asn Gln Ala Leu Leu Asn Ala Arg
50 55 60
Asp Glu Leu Gln Ala Gln Ile Asp Lys Trp His Arg Arg Arg Val Ile
65 70 75 80
Glu Pro Ile Asp Met Asp Ala Tyr Arg Gln Phe Leu Thr Glu Ile Gly
85 90 95
Tyr Leu Leu Pro Glu Pro Asp Asp Phe Thr Ile Thr Thr Ser Gly Val
100 105 110
Asp Ala Glu Ile Thr Thr Thr Ala Gly Pro Gln Leu Val Val Pro Val
115 120 125
Leu Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser
130 135 140
Leu Tyr Asp Ala Leu Tyr Gly Thr Asp Val Ile Pro Glu Thr Asp Gly
145 150 155 160
Ala Glu Lys Gly Pro Thr Tyr Asn Lys Val Arg Gly Asp Lys Val Ile
165 170 175
Ala Tyr Ala Arg Lys Phe Leu Asp Asp Ser Val Pro Leu Ser Ser Gly
180 185 190
Ser Phe Gly Asp Ala Thr Gly Phe Thr Val Gln Asp Gly Gln Leu Val
195 200 205
Val Ala Leu Pro Asp Lys Ser Thr Gly Leu Ala Asn Pro Gly Gln Phe
210 215 220
Ala Gly Tyr Thr Gly Ala Ala Glu Ser Pro Thr Ser Val Leu Leu Ile
225 230 235 240
Asn His Gly Leu His Ile Glu Ile Leu Ile Asp Pro Glu Ser Gln Val
245 250 255
Gly Thr Thr Asp Arg Ala Gly Val Lys Asp Val Ile Leu Glu Ser Ala
260 265 270
Ile Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala
275 280 285
Ala Asp Lys Val Leu Gly Tyr Arg Asn Trp Leu Gly Leu Asn Lys Gly
290 295 300
Asp Leu Ala Ala Ala Val Asp Lys Asp Gly Thr Ala Phe Leu Arg Val
305 310 315 320

Leu Asn Arg Asp Arg Asn Tyr Thr Ala Pro Gly Gly Gly Gln Phe Thr
 325 330 335
 Leu Pro Gly Arg Ser Leu Met Phe Val Arg Asn Val Gly His Leu Met
 340 345 350
 Thr Asn Asp Ala Ile Val Asp Thr Asp Gly Ser Glu Val Phe Glu Gly
 355 360 365
 Ile Met Asp Ala Leu Phe Thr Gly Leu Ile Ala Ile His Gly Leu Lys
 370 375 380
 Ala Ser Asp Val Asn Gly Pro Leu Ile Asn Ser Arg Thr Gly Ser Ile
 385 390 395 400
 Tyr Ile Val Lys Pro Lys Met His Gly Pro Ala Glu Val Ala Phe Thr
 405 410 415
 Cys Glu Leu Phe Ser Arg Val Glu Asp Val Leu Gly Leu Pro Gln Asn
 420 425 430
 Thr Met Lys Ile Gly Ile Met Asp Glu Glu Arg Arg Thr Thr Val Asn
 435 440 445
 Leu Lys Ala Cys Ile Lys Ala Ala Ala Asp Arg Val Val Phe Ile Asn
 450 455 460
 Thr Gly Phe Leu Asp Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu
 465 470 475 480
 Ala Gly Pro Met Val Arg Lys Gly Thr Met Lys Ser Gln Pro Trp Ile
 485 490 495
 Leu Ala Tyr Glu Asp His Asn Val Asp Ala Gly Leu Ala Ala Gly Phe
 500 505 510
 Ser Gly Arg Ala Gln Val Gly Lys Gly Met Trp Thr Met Thr Glu Leu
 515 520 525
 Met Ala Asp Met Val Glu Thr Lys Ile Ala Gln Pro Arg Ala Gly Ala
 530 535 540
 Ser Thr Ala Trp Val Pro Ser Pro Thr Ala Ala Thr Leu His Ala Leu
 545 550 555 560
 His Tyr His Gln Val Asp Val Ala Ala Val Gln Gln Gly Leu Ala Gly
 565 570 575
 Lys Arg Arg Ala Thr Ile Glu Gln Leu Leu Thr Ile Pro Leu Ala Lys
 580 585 590
 Glu Leu Ala Trp Ala Pro Asp Glu Ile Arg Glu Glu Val Asp Asn Asn
 595 600 605
 Cys Gln Ser Ile Leu Gly Tyr Val Val Arg Trp Val Asp Gln Gly Val
 610 615 620
 Gly Cys Ser Lys Val Pro Asp Ile His Asp Val Ala Leu Met Glu Asp
 625 630 635 640

Arg Ala Thr Leu Arg Ile Ser Ser Gln Leu Leu Ala Asn Trp Leu Arg
 645 650 655
 His Gly Val Ile Thr Ser Ala Asp Val Arg Ala Ser Leu Glu Arg Met
 660 665 670
 Ala Pro Leu Val Asp Arg Gln Asn Ala Gly Asp Val Ala Tyr Arg Pro
 675 680 685
 Met Ala Pro Asn Phe Asp Asp Ser Ile Ala Phe Leu Ala Ala Gln Glu
 690 695 700
 Leu Ile Leu Ser Gly Ala Gln Gln Pro Asn Gly Tyr Thr Glu Pro Ile
 705 710 715 720
 Leu His Arg Arg Arg Arg Glu Phe Lys Ala Arg Ala Ala Glu Lys Pro
 725 730 735
 Ala Pro Ser Asp Arg Ala Gly Asp Asp Ala Ala Arg Val Gln Lys Tyr
 740 745 750
 Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg Val Ala Glu
 755 760 765
 Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val Val Val Val
 770 775 780
 Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu Ala Gln Gln
 785 790 795 800
 Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu Leu Thr Ala
 805 810 815
 Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile Glu Ser Leu
 820 825 830
 Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly Val Ile Thr
 835 840 845
 Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr Pro Gly Arg
 850 855 860
 Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu Val Ala Gly Phe
 865 870 875 880
 Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu Gly Arg Gly
 885 890 895
 Gly Ser Asp Thr Thr Ala Val Ala Met Ala Ala Ala Leu Gly Ala Asp
 900 905 910
 Val Cys Glu Ile Tyr Thr Asp Val Asp Gly Ile Phe Ser Ala Asp Pro
 915 920 925
 Arg Ile Val Arg Asn Ala Arg Lys Leu Asp Thr Val Thr Phe Glu Glu
 930 935 940
 Met Leu Glu Met Ala Ala Cys Gly Ala Lys Val Leu Met Leu Arg Cys
 945 950 955 960

Val Glu Tyr Ala Arg Arg His Asn Ile Pro Val His Val Arg Ser Ser
 965 970 975
 Tyr Ser Asp Arg Pro Gly Thr Val Val Val Gly Ser Ile Lys Asp Val
 980 985 990
 Pro Met Glu Asp Pro Ile Leu Thr Gly Val Ala His Asp Arg Ser Glu
 995 1000 1005
 Ala Lys Val Thr Ile Val Gly Leu Pro Asp Ile Pro Gly Tyr Ala Ala
 1010 1015 1020
 Lys Val Phe Arg Ala Val Ala Arg Arg Arg Arg Gln His Arg His Gly
 1025 1030 1035 1040
 Ala Ala Glu Arg Leu Gln Gly Arg Gly Arg Gln Asp Arg His His Leu
 1045 1050 1055
 His Leu Leu Pro Gln Thr Ser Gly Pro Pro Pro Trp Lys Asn Trp Thr
 1060 1065 1070
 Arg Ser Glu Thr Arg Ser Ala Ser Thr Gln Leu Leu Tyr Asp Asp His
 1075 1080 1085
 Ile Gly Lys Val Ser Leu Ile Gly Ala Gly Met Arg Ser His Pro Gly
 1090 1095 1100
 Val Thr Ala Thr Phe Cys Glu Ala Leu Ala Ala Val Gly Val Asn Ile
 1105 1110 1115 1120
 Glu Leu Ile Ser Thr Ser Glu Asp Gln Arg Ser Arg Cys Cys Ala Ala
 1125 1130 1135
 Thr Pro Asn Trp Thr Arg Pro Trp Ser Arg Cys Met Lys Arg Ser Gly
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 Ser Ala Ala Thr Arg Arg Pro Arg Cys Thr Arg Gly Arg Asp Gly Arg
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 Trp Ala Cys Gln
 1170

<210> 53

<211> 2952

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:TbF15 fusion protein

<400> 53

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 gctcgggtca ttgagcagga catggccgtg gacagcgccg gcaagatcac ctaccgcac 180
 aagctcgaag tgtcgttcaa gatgaggccg gcgcaaccga ggtgtggctc gaaaccaccg 240
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 ccggtgacgt tggcggagac cggtagcacg ctgctctacc cgctgttcaa cctgtgggg 360
 ccggcctttc acgagaggta tccgaacgtc acgatcaccg ctcagggcac cggttctggt 420
 gccgggatcg cgcaggccgc cgccgggacg gtcaacattg ggcctccga cgcctatctg 480

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cagcagggtca actacaacct gcccggagtg agcagacc tcaagctgaa cggaaaagtc 600
ctggcgggcca tgtaccaggg caccatcaaa acctgggacg acccgcatat cgctgcgctc 660
aaccccgcg tgaacctgcc cggcaccgcg gtagttccgc tgcaccgctc cgacgggttc 720
ggtgacacct tcttgttcac ccagtacctg tccaagcaag atcccgaggg ctgggggcaag 780
tcgcccggct tcggcaccac cgtcgacttc ccggcggtgc cgggtgcgct gggtgagaac 840
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catcagggac aagggggcgc caagtccaag ggttctcagc aggaagacga ggcgctctac 2880
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gagtcgaagt ga 2952

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<210> 54
<211> 983
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:TbF15 fusion
      protein

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Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
      20              25              30

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Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
 35 40 45
 Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
 50 55 60
 Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Cys Gly Ser Lys Pro Pro
 65 70 75 80
 Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr
 85 90 95
 Pro Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu
 100 105 110
 Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro
 115 120 125
 Asn Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala
 130 135 140
 Gln Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu
 145 150 155 160
 Ser Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu
 165 170 175
 Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu
 180 185 190
 His Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr
 195 200 205
 Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val
 210 215 220
 Asn Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser
 225 230 235 240
 Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu
 245 250 255
 Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala
 260 265 270
 Val Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly
 275 280 285
 Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu
 290 295 300
 Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser
 305 310 315 320
 Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala
 325 330 335
 Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile
 340 345 350

Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala
 355 360 365
 Ile Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln
 370 375 380
 Ala Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu
 385 390 395 400
 Asp Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser
 405 410 415
 Asp Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala
 420 425 430
 Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp
 435 440 445
 Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln
 450 455 460
 Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val
 465 470 475 480
 Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile
 485 490 495
 Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu
 500 505 510
 Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Thr Gln Ser Gln
 515 520 525
 Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn Arg Ala Asn Glu Val
 530 535 540
 Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val Pro Ile Thr Pro Cys
 545 550 555 560
 Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln Leu Val Leu Ser Ala
 565 570 575
 Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala Lys Glu Arg Gln Arg
 580 585 590
 Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala Tyr Gly Glu Val Asp
 595 600 605
 Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly Glu Gly Thr Val Gln
 610 615 620
 Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser Ser Ala Glu Leu Thr
 625 630 635 640
 Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro Asn Phe Met Asp Leu
 645 650 655
 Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp Gln Gly Ala Ser Leu
 660 665 670

Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn Leu Thr Leu Gln Gly
 675 680 685
 Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp Glu Gly Asp Ala Ala
 690 695 700
 Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg Gln Trp Ile Leu His
 705 710 715 720
 Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln Ala Gln Tyr Val Ala
 725 730 735
 Gln Leu His Val Trp Ala Arg Arg Glu His Pro Thr Tyr Glu Asp Ile
 740 745 750
 Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro Ser Ala Arg Asp Gln
 755 760 765
 Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg Ser Glu Lys Val Leu
 770 775 780
 Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro Val Asn Pro Pro Lys
 785 790 795 800
 Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro Pro Gln Glu Gln
 805 810 815
 Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser Asp Gly Ser Gly Val
 820 825 830
 Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met Val Pro Pro Thr Gly
 835 840 845
 Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala Ala Gln Leu Thr Ser
 850 855 860
 Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp Val Ala Val Lys Ala
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 Ala Ser Leu Gly Gly Gly Gly Gly Gly Gly Val Pro Ser Ala Pro Leu
 885 890 895
 Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg Pro Ala Gly Ala Gly
 900 905 910
 Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly Gly Gly Ala Ala Leu
 915 920 925
 Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala Ala His Gln Gly Gln
 930 935 940
 Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu Asp Glu Ala Leu Tyr
 945 950 955 960
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 965 970 975
 Gln Asp Ser Lys Glu Ser Lys
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<210> 55

<400> 55

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<210> 56

<400> 56

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<210> 57

<211> 2232

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:fusion protein
HTCC#1(184-392)-TbH9-HTCC#1(1-129)

<220>

<221> CDS

<222> (4)..(2226)

<400> 57

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Thr Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu	
20 25 30	
aaa gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct	144
Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser	
35 40 45	
cga ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg	192
Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu	
50 55 60	
acc ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg	240
Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala	
65 70 75	
gcc ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg	288
Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala	
80 85 90 95	
agc tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt	336
Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly	
100 105 110	
ttt ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg	384
Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg	
115 120 125	

cag gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag	432
Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu	
130 135 140	
cag gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt	480
Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly	
145 150 155	
atg ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg	528
Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala	
160 165 170 175	
tcg aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc	576
Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly	
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act gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg	624
Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly	
195 200 205	
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Gln Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly	
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gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt	720
Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly	
225 230 235	
tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt	768
Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser	
240 245 250 255	
gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg	816
Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu	
260 265 270	
acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg	864
Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala	
275 280 285	
gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag	912
Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu	
290 295 300	
ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg	960
Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala	
305 310 315	
tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa	1008
Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu	
320 325 330 335	
ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg	1056
Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala	
340 345 350	
atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc	1104
Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala	
355 360 365	

gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg gcg acg gcg acg	1152
Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr	
370 375 380	
ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc	1200
Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu	
385 390 395	
ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg	1248
Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala	
400 405 410 415	
aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag	1296
Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln	
420 425 430	
ccc acg cag ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag	1344
Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys	
435 440 445	
acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc	1392
Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala	
450 455 460	
aac aac cac atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc	1440
Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr	
465 470 475	
ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag gcc	1488
Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala	
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Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly	
500 505 510	
agc tcg ctg ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg	1584
Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu	
515 520 525	
ggt cgg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc	1632
Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala	
530 535 540	
gcg gcc aac cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg ctg acc	1680
Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr	
545 550 555	
agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg	1728
Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly	
560 565 570 575	
ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt	1776
Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly	
580 585 590	
gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca	1824
Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala	
595 600 605	

gcc ggc gat atc atg agc aga gcg ttc atc atc gat cca acg atc agt 1872
 Ala Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser
 610 615 620

 gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa 1920
 Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln
 625 630 635

 ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag 1968
 Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu
 640 645 650 655

 gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg 2016
 Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala
 660 665 670

 gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa 2064
 Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu
 675 680 685

 ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac gac cag gcc 2112
 Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala
 690 695 700

 aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt 2160
 Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly
 705 710 715

 ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc 2208
 Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val
 720 725 730 735

 gtc ggg cac gcc cta taa gatatc 2232
 Val Gly His Ala Leu
 740

<210> 58
 <211> 740
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fusion protein
 HTCC#1(184-392)-TbH9-HTCC#1(1-129)

<400> 58
 Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Thr
 1 5 10 15
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 20 25 30
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 35 40 45
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 50 55 60
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 65 70 75 80

Gly	Leu	Ser	Ala	Ser	Ser	Gly	Leu	Ala	His	Ala	Asp	Ser	Leu	Ala	Ser	
85								90				95				
Ser	Ala	Ser	Leu	Pro	Ala	Leu	Ala	Gly	Ile	Gly	Gly	Gly	Ser	Gly	Phe	
100								105				110				
Gly	Gly	Leu	Pro	Ser	Leu	Ala	Gln	Val	His	Ala	Ala	Ser	Thr	Arg	Gln	
115								120				125				
Ala	Leu	Arg	Pro	Arg	Ala	Asp	Gly	Pro	Val	Gly	Ala	Ala	Ala	Glu	Gln	
130								135				140				
Val	Gly	Gly	Gln	Ser	Gln	Leu	Val	Ser	Ala	Gln	Gly	Ser	Gln	Gly	Met	
145								150				155				
Gly	Gly	Pro	Val	Gly	Met	Gly	Gly	Met	His	Pro	Ser	Ser	Gly	Ala	Ser	
				165				170				175				
Lys	Gly	Thr	Thr	Thr	Lys	Lys	Tyr	Ser	Glu	Gly	Ala	Ala	Ala	Gly	Thr	
				180				185				190				
Glu	Asp	Ala	Glu	Arg	Ala	Pro	Val	Glu	Ala	Asp	Ala	Gly	Gly	Gly	Gln	
				195				200				205				
Lys	Val	Leu	Val	Arg	Asn	Val	Val	Glu	Phe	Met	Val	Asp	Phe	Gly	Ala	
210								215				220				
Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met	Tyr	Ala	Gly	Pro	Gly	Ser	
225								230				235				
Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp	Asp	Ser	Val	Ala	Ser	Asp	
				245				250				255				
Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser	Val	Val	Trp	Gly	Leu	Thr	
				260				265				270				
Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	Leu	Met	Val	Ala	Ala	Ala	
				275				280				285				
Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	Gln	Ala	Glu	Leu	
290								295				300				
Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	Glu	Thr	Ala	Tyr	
305								310				315				
Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	Arg	Ala	Glu	Leu	
				325				330				335				
Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	Thr	Pro	Ala	Ile	
				340				345				350				
Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	Gln	Asp	Ala	Ala	
				355				360				365				
Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Thr	Leu	
370								375				380				
Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	Gly	Gly	Leu	Leu	
385								390				395				
												400				

Glu Gln Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn
 405 410 415
 Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro
 420 425 430
 Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr
 435 440 445
 Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn
 450 455 460
 Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu
 465 470 475 480
 Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val
 485 490 495
 Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser
 500 505 510
 Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly
 515 520 525
 Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala
 530 535 540
 Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser
 545 550 555 560
 Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu
 565 570 575
 Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val
 580 585 590
 Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala
 595 600 605
 Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala
 610 615 620
 Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
 625 630 635 640
 Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu
 645 650 655
 Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp
 660 665 670
 Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu
 675 680 685
 Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn
 690 695 700
 Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu
 705 710 715 720

Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val
725 730 735

Gly His Ala Leu
740

<210> 59
<211> 2365
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
HTCC#1(1-149)-TbH9-HTCC#1(161-392)

<220>
<221> CDS
<222> (4) .. (2355)

<400> 59
cat atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat 48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp
1 5 10 15
cca acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga 96
Pro Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly
20 25 30
ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa 144
Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu
35 40 45
aaa gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta 192
Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu
50 55 60
ggt tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat 240
Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn
65 70 75
ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc 288
Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile
80 85 90 95
cac gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc 336
His Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly
100 105 110
gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc 384
Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr
115 120 125
tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg 432
Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro
130 135 140
ttt tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt aag ctt atg 480
Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Met
145 150 155

gtg gat ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg tac	528
Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr	
160 165 170 175	
gcc ggc ccg ggt tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac	576
Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp	
180 185 190	
agc gtg gcg agt gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg	624
Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val	
195 200 205	
gtc tgg ggt ctg acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg	672
Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu	
210 215 220	
atg gtg gcg gcg gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg	720
Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala	
225 230 235	
ggg cag gcc gag ctg acc gcc gcc cag gtc ccg gtt gct gcg gcg gcc	768
Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala	
240 245 250 255	
tac gag acg gcg tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag	816
Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu	
260 265 270	
aac cgt gct gaa ctg atg att ctg ata gcg acc aac ctc ttg ggg caa	864
Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln	
275 280 285	
aac acc ccg gcg atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg	912
Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp	
290 295 300	
gcc caa gac gcc gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg	960
Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr	
305 310 315	
gcg acg gcg acg ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc	1008
Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser	
320 325 330 335	
gcg ggt ggg ctc ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac	1056
Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp	
340 345 350	
acc gcc gcg gcg aac cag ttg atg aac aat gtg ccc cag gcg ctg caa	1104
Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln	
355 360 365	
cag ctg gcc cag ccc acg cag ggc acc acg cct tct tcc aag ctg ggt	1152
Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly	
370 375 380	
ggc ctg tgg aag acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg	1200
Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met	
385 390 395	

gtg	tcg	atg	gcc	aac	aac	cac	atg	tcg	atg	acc	aac	tcg	ggt	gtg	tcg	1248
Val	Ser	Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	
400					405					410					415	
atg	acc	aac	acc	ttg	agc	tcg	atg	ttg	aag	ggc	ttt	gct	ccg	gcg	gcg	1296
Met	Thr	Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	
				420					425						430	
gcc	gcc	cag	gcc	gtg	caa	acc	gcg	gcg	caa	aac	ggg	gtc	ccg	gcg	atg	1344
Ala	Ala	Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	
			435					440					445			
agc	tcg	ctg	ggc	agc	tcg	ctg	ggt	tct	tcg	ggt	ctg	ggc	ggt	ggg	gtg	1392
Ser	Ser	Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	Val	
		450					455					460				
gcc	gcc	aac	ttg	ggt	cgg	gcg	gcc	tcg	gtc	ggt	tcg	ttg	tcg	gtg	ccg	1440
Ala	Ala	Asn	Leu	Gly	Arg	Ala	Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	Pro	
		465				470					475					
cag	gcc	tgg	gcc	gcg	gcc	aac	cag	gca	gtc	acc	ccg	gcg	gcg	cgg	gcg	1488
Gln	Ala	Trp	Ala	Ala	Ala	Asn	Gln	Ala	Val	Thr	Pro	Ala	Ala	Arg	Ala	
480					485					490					495	
ctg	ccg	ctg	acc	agc	ctg	acc	agc	gcc	gcg	gaa	aga	ggg	ccc	ggg	cag	1536
Leu	Pro	Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly	Gln	
				500					505					510		
atg	ctg	ggc	ggg	ctg	ccg	gtg	ggg	cag	atg	ggc	gcc	agg	gcc	ggt	ggt	1584
Met	Leu	Gly	Gly	Leu	Pro	Val	Gly	Gln	Met	Gly	Ala	Arg	Ala	Gly	Gly	
			515				520						525			
ggg	ctc	agt	ggt	gtg	ctg	cgt	gtt	ccg	ccg	cga	ccc	tat	gtg	atg	ccg	1632
Gly	Leu	Ser	Gly	Val	Leu	Arg	Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	Pro	
		530					535					540				
cat	tct	ccg	gca	gcc	ggc	aag	ctt	act	caa	ctc	ctc	aaa	ttg	ctt	gcc	1680
His	Ser	Pro	Ala	Ala	Gly	Lys	Leu	Thr	Gln	Leu	Leu	Lys	Leu	Leu	Ala	
		545				550					555					
aaa	ttg	gcg	gag	ttg	gtc	gcg	gcc	gcc	att	gcg	gac	atc	att	tcg	gat	1728
Lys	Leu	Ala	Glu	Leu	Val	Ala	Ala	Ala	Ile	Ala	Asp	Ile	Ile	Ser	Asp	
560					565				570						575	
gtg	gcg	gac	atc	atc	aag	ggc	atc	ctc	gga	gaa	gtg	tgg	gag	ttc	atc	1776
Val	Ala	Asp	Ile	Ile	Lys	Gly	Ile	Leu	Gly	Glu	Val	Trp	Glu	Phe	Ile	
				580					585					590		
aca	aac	gcg	ctc	aac	ggc	ctg	aaa	gag	ctt	tgg	gac	aag	ctc	acg	ggg	1824
Thr	Asn	Ala	Leu	Asn	Gly	Leu	Lys	Glu	Leu	Trp	Asp	Lys	Leu	Thr	Gly	
			595					600					605			
tgg	gtg	acc	gga	ctg	ttc	tct	cga	ggg	tgg	tcg	aac	ctg	gag	tcc	ttc	1872
Trp	Val	Thr	Gly	Leu	Phe	Ser	Arg	Gly	Trp	Ser	Asn	Leu	Glu	Ser	Phe	
		610					615					620				
ttt	gcg	ggc	gtc	ccc	ggc	ttg	acc	ggc	gcg	acc	agc	ggc	ttg	tcg	caa	1920
Phe	Ala	Gly	Val	Pro	Gly	Leu	Thr	Gly	Ala	Thr	Ser	Gly	Leu	Ser	Gln	
	625					630					635					

gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca tcg tcg ggc ttg	1968
Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu	
640 645 650 655	
gct cac gcg gat agc ctg gcg agc tca gcc agc ttg ccc gcc ctg gcc	2016
Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala	
660 665 670	
ggc att ggg ggc ggg tcc ggt ttt ggg ggc ttg ccg agc ctg gct cag	2064
Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln	
675 680 685	
gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc cga gct gat ggc	2112
Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly	
690 695 700	
ccg gtc ggc gcc gct gcc gag cag gtc ggc ggg cag tcg cag ctg gtc	2160
Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val	
705 710 715	
tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta ggc atg ggc ggc	2208
Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly	
720 725 730 735	
atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg acg aag aag tac	2256
Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr	
740 745 750	
tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag cgc gcg cca gtc	2304
Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val	
755 760 765	
gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta cga aac gtc gtc	2352
Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val	
770 775 780	
taa cggcgaattc	2365

<210> 60

<211> 783

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:fusion protein
HTCC#1(1-149)-TbH9-HTCC#1(161-392)

<400> 60

Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
1 5 10 15

Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
20 25 30

Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
35 40 45

Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
50 55 60

Ser	Ala	Ala	Asp	Lys	Tyr	Ala	Gly	Lys	Asn	Arg	Asn	His	Val	Asn	Phe	65	70	75	80
Phe	Gln	Glu	Leu	Ala	Asp	Leu	Asp	Arg	Gln	Leu	Ile	Ser	Leu	Ile	His	85	90	95	
Asp	Gln	Ala	Asn	Ala	Val	Gln	Thr	Thr	Arg	Asp	Ile	Leu	Glu	Gly	Ala	100	105	110	
Lys	Lys	Gly	Leu	Glu	Phe	Val	Arg	Pro	Val	Ala	Val	Asp	Leu	Thr	Tyr	115	120	125	
Ile	Pro	Val	Val	Gly	His	Ala	Leu	Ser	Ala	Ala	Phe	Gln	Ala	Pro	Phe	130	135	140	
Cys	Ala	Gly	Ala	Met	Ala	Val	Val	Gly	Gly	Ala	Leu	Lys	Leu	Met	Val	145	150	155	160
Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met	Tyr	Ala	165	170	175	
Gly	Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp	Asp	Ser	180	185	190	
Val	Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser	Val	Val	195	200	205	
Trp	Gly	Leu	Thr	Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	Leu	Met	210	215	220	
Val	Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	225	230	235	240
Gln	Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	245	250	255	
Glu	Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	260	265	270	
Arg	Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	275	280	285	
Thr	Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	290	295	300	
Gln	Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	305	310	315	320
Thr	Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	325	330	335	
Gly	Gly	Leu	Leu	Glu	Gln	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	340	345	350	
Ala	Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	Gln	Gln	355	360	365	
Leu	Ala	Gln	Pro	Thr	Gln	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	370	375	380	

Leu	Trp	Lys	Thr	Val	Ser	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	385	390	395	400
Ser	Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	405	410	415	
Thr	Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	420	425	430	
Ala	Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	435	440	445	
Ser	Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	Val	Ala	450	455	460	
Ala	Asn	Leu	Gly	Arg	Ala	Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	Pro	Gln	465	470	475	480
Ala	Trp	Ala	Ala	Ala	Asn	Gln	Ala	Val	Thr	Pro	Ala	Ala	Arg	Ala	Leu	485	490	495	
Pro	Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly	Gln	Met	500	505	510	
Leu	Gly	Gly	Leu	Pro	Val	Gly	Gln	Met	Gly	Ala	Arg	Ala	Gly	Gly	Gly	515	520	525	
Leu	Ser	Gly	Val	Leu	Arg	Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	Pro	His	530	535	540	
Ser	Pro	Ala	Ala	Gly	Lys	Leu	Thr	Gln	Leu	Leu	Lys	Leu	Leu	Ala	Lys	545	550	555	560
Leu	Ala	Glu	Leu	Val	Ala	Ala	Ala	Ile	Ala	Asp	Ile	Ile	Ser	Asp	Val	565	570	575	
Ala	Asp	Ile	Ile	Lys	Gly	Ile	Leu	Gly	Glu	Val	Trp	Glu	Phe	Ile	Thr	580	585	590	
Asn	Ala	Leu	Asn	Gly	Leu	Lys	Glu	Leu	Trp	Asp	Lys	Leu	Thr	Gly	Trp	595	600	605	
Val	Thr	Gly	Leu	Phe	Ser	Arg	Gly	Trp	Ser	Asn	Leu	Glu	Ser	Phe	Phe	610	615	620	
Ala	Gly	Val	Pro	Gly	Leu	Thr	Gly	Ala	Thr	Ser	Gly	Leu	Ser	Gln	Val	625	630	635	640
Thr	Gly	Leu	Phe	Gly	Ala	Ala	Gly	Leu	Ser	Ala	Ser	Ser	Gly	Leu	Ala	645	650	655	
His	Ala	Asp	Ser	Leu	Ala	Ser	Ser	Ala	Ser	Leu	Pro	Ala	Leu	Ala	Gly	660	665	670	
Ile	Gly	Gly	Gly	Ser	Gly	Phe	Gly	Gly	Leu	Pro	Ser	Leu	Ala	Gln	Val	675	680	685	
His	Ala	Ala	Ser	Thr	Arg	Gln	Ala	Leu	Arg	Pro	Arg	Ala	Asp	Gly	Pro	690	695	700	

Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val Ser
705 710 715 720

Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met
725 730 735

His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser
740 745 750

Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu
755 760 765

Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
770 775 780

<210> 61
<211> 2445
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
HTCC#1(184-392)-TbH9-HTCC#1(1-200)

<220>
<221> CDS
<222> (4) .. (2439)

<400> 61
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1 5 10 15

atc ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg 96
Ile Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu
20 25 30

aaa gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct 144
Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser
35 40 45

cga ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg 192
Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu
50 55 60

acc ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg 240
Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala
65 70 75

gcc ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg 288
Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala
80 85 90 95

agc tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt 336
Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly
100 105 110

ttt ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg 384
Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg
115 120 125

cag gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag	432
Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu	
130 135 140	
cag gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt	480
Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly	
145 150 155	
atg ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg	528
Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala	
160 165 170 175	
tcg aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc	576
Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly	
180 185 190	
act gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg	624
Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly	
195 200 205	
caa aag gtg ctg gta cga aac gtc gtc gaa ttc atg gtg gat ttc ggg	672
Gln Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly	
210 215 220	
gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt	720
Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly	
225 230 235	
tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt	768
Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser	
240 245 250 255	
gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg	816
Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu	
260 265 270	
acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg	864
Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala	
275 280 285	
gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag	912
Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu	
290 295 300	
ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg	960
Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala	
305 310 315	
tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa	1008
Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu	
320 325 330 335	
ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg	1056
Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala	
340 345 350	
atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc	1104
Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala	
355 360 365	

gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg gcg acg gcg acg	1152
Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr	
370 375 380	
ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc	1200
Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu	
385 390 395	
ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg	1248
Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala	
400 405 410 415	
aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag	1296
Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln	
420 425 430	
ccc acg cag ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag	1344
Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys	
435 440 445	
acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc	1392
Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala	
450 455 460	
aac aac cac atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc	1440
Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr	
465 470 475	
ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag gcc	1488
Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala	
480 485 490 495	
gtg caa acc gcg gcg caa aac ggg gtc cgg gcg atg agc tcg ctg ggc	1536
Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly	
500 505 510	
agc tcg ctg ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg	1584
Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu	
515 520 525	
ggt cgg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc	1632
Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala	
530 535 540	
gcg gcc aac cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg ctg acc	1680
Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr	
545 550 555	
agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg	1728
Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly	
560 565 570 575	
ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt	1776
Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly	
580 585 590	
gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca	1824
Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala	
595 600 605	

gcc ggc gat atc atg agc aga gcg ttc atc atc gat cca acg atc agt	1872
Ala Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser	
610 615 620	
gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa	1920
Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln	
625 630 635	
ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag	1968
Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu	
640 645 650 655	
gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg	2016
Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala	
660 665 670	
gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa	2064
Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu	
675 680 685	
ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac gac cag gcc	2112
Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala	
690 695 700	
aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt	2160
Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly	
705 710 715	
ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc	2208
Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val	
720 725 730 735	
gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg ttt tgc gcg ggc	2256
Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly	
740 745 750	
gcg atg gcc gta gtg ggc ggc gcg ctt gcc tac ttg gtc gtg aaa acg	2304
Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr	
755 760 765	
ctg atc aac gcg act caa ctc ctc aaa ttg ctt gcc aaa ttg gcg gag	2352
Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu	
770 775 780	
ttg gtc gcg gcc gcc att gcg gac atc att tcg gat gtg gcg gac atc	2400
Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile	
785 790 795	
atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc taa gatatc	2445
Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile	
800 805 810	

<210> 62

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:fusion protein

HTCC#1(184-392)-TbH9-HTCC#1(1-200)

<400> 62

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Leu	Gly	Glu	Val	Trp	Glu	Phe	Ile	Thr	Asn	Ala	Leu	Asn	Gly	Leu	Lys
			20					25					30		
Glu	Leu	Trp	Asp	Lys	Leu	Thr	Gly	Trp	Val	Thr	Gly	Leu	Phe	Ser	Arg
		35					40					45			
Gly	Trp	Ser	Asn	Leu	Glu	Ser	Phe	Phe	Ala	Gly	Val	Pro	Gly	Leu	Thr
	50					55					60				
Gly	Ala	Thr	Ser	Gly	Leu	Ser	Gln	Val	Thr	Gly	Leu	Phe	Gly	Ala	Ala
65					70					75					80
Gly	Leu	Ser	Ala	Ser	Ser	Gly	Leu	Ala	His	Ala	Asp	Ser	Leu	Ala	Ser
				85					90					95	
Ser	Ala	Ser	Leu	Pro	Ala	Leu	Ala	Gly	Ile	Gly	Gly	Gly	Ser	Gly	Phe
			100					105					110		
Gly	Gly	Leu	Pro	Ser	Leu	Ala	Gln	Val	His	Ala	Ala	Ser	Thr	Arg	Gln
		115					120					125			
Ala	Leu	Arg	Pro	Arg	Ala	Asp	Gly	Pro	Val	Gly	Ala	Ala	Ala	Glu	Gln
	130					135					140				
Val	Gly	Gly	Gln	Ser	Gln	Leu	Val	Ser	Ala	Gln	Gly	Ser	Gln	Gly	Met
145					150					155					160
Gly	Gly	Pro	Val	Gly	Met	Gly	Gly	Met	His	Pro	Ser	Ser	Gly	Ala	Ser
				165					170					175	
Lys	Gly	Thr	Thr	Thr	Lys	Lys	Tyr	Ser	Glu	Gly	Ala	Ala	Ala	Gly	Thr
			180					185					190		
Glu	Asp	Ala	Glu	Arg	Ala	Pro	Val	Glu	Ala	Asp	Ala	Gly	Gly	Gly	Gln
	195						200					205			
Lys	Val	Leu	Val	Arg	Asn	Val	Val	Glu	Phe	Met	Val	Asp	Phe	Gly	Ala
	210				215						220				
Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met	Tyr	Ala	Gly	Pro	Gly	Ser
225					230					235					240
Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp	Asp	Ser	Val	Ala	Ser	Asp
				245					250					255	
Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser	Val	Val	Trp	Gly	Leu	Thr
			260					265					270		
Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	Leu	Met	Val	Ala	Ala	Ala
		275					280					285			
Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	Gln	Ala	Glu	Leu
	290					295					300				
Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	Glu	Thr	Ala	Tyr
305					310					315					320

Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu
 325 330 335
 Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile
 340 345 350
 Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala
 355 360 365
 Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu
 370 375 380
 Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu
 385 390 395 400
 Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn
 405 410 415
 Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro
 420 425 430
 Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr
 435 440 445
 Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn
 450 455 460
 Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu
 465 470 475 480
 Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val
 485 490 495
 Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser
 500 505 510
 Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly
 515 520 525
 Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala
 530 535 540
 Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser
 545 550 555 560
 Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu
 565 570 575
 Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val
 580 585 590
 Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala
 595 600 605
 Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala
 610 615 620
 Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
 625 630 635 640

Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu
 645 650 655
 Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp
 660 665 670
 Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu
 675 680 685
 Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn
 690 695 700
 Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu
 705 710 715 720
 Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val
 725 730 735
 Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala
 740 745 750
 Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu
 755 760 765
 Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu
 770 775 780
 Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile
 785 790 795 800
 Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile
 805 810

<210> 63
 <211> 1629
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: fusion protein
 TbRa12-HTCC#1

<220>
 <221> CDS
 <222> (4) .. (1623)

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 ctg tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg 96
 Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met
 20 25 30
 gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat 144
 Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His
 35 40 45

atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc	192
Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly	
50 55 60	
aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt	240
Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser	
65 70 75	
ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg	288
Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro	
80 85 90 95	
atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc	336
Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro	
100 105 110	
ggg gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt	384
Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg	
115 120 125	
aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc cta gta	432
Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Leu Val	
130 135 140	
cct aga ggt tca atg agc aga gcg ttc atc atc gat cca acg atc agt	480
Pro Arg Gly Ser Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser	
145 150 155	
gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa	528
Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln	
160 165 170 175	
ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag	576
Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu	
180 185 190	
gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg	624
Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala	
195 200 205	
gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa	672
Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu	
210 215 220	
ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac gac cag gcc	720
Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala	
225 230 235	
aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt	768
Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly	
240 245 250 255	
ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc	816
Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val	
260 265 270	
gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg ttt tgc gcg ggc	864
Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly	
275 280 285	

gcg atg gcc gta gtg ggc ggc gcg ctt gcc tac ttg gtc gtg aaa acg Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr 290 295 300	912
ctg atc aac gcg act caa ctc ctc aaa ttg ctt gcc aaa ttg gcg gag Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu 305 310 315	960
ttg gtc gcg gcc gcc att gcg gac atc att tcg gat gtg gcg gac atc Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile 320 325 330 335	1008
atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu 340 345 350	1056
aac ggc ctg aaa gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly 355 360 365	1104
ctg ttc tct cga ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val 370 375 380	1152
ccc ggc ttg acc ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu 385 390 395	1200
ttc ggt gcg gcc ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp 400 405 410 415	1248
agc ctg gcg agc tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly 420 425 430	1296
ggg tcc ggt ttt ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala 435 440 445	1344
tca act cgg cag gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala 450 455 460	1392
gct gcc gag cag gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly 465 470 475	1440
tcc caa ggt atg ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser 480 485 490 495	1488
tcg ggg gcg tcg aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala 500 505 510	1536
gcg gcg ggc act gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala 515 520 525	1584

ggc ggt ggg caa aag gtg ctg gta cga aac gtc gtc taa gaattc 1629
 Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
 530 535 540

<210> 64
 <211> 539
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fusion protein
 TbRa12-HTCC#1

<400> 64
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 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
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 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
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<223> Description of Artificial Sequence:vector encoding
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:region encoding
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<223> Description of Artificial Sequence:vector encoding
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mapping

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<210> 96
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sequence of HTCC#1 peptide 10 for T-cell epitope
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<210> 108
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<210> 111

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<212> DNA

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<212> DNA

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<212> DNA

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<210> 114

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<210> 115
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<210> 116
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<210> 117
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<400> 117
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<210> 118
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<212> DNA
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 <210> 122
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 <210> 123
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
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 sequence of HTCC#1 peptide 30 for T-cell epitope
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<400> 123
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<210> 124
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 Leu Tyr Asp Leu
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<210> 125
 <211> 20
 <212> PRT
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<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
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<400> 125
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 1 5 10 15
 Gly Ile Leu Tyr
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<210> 126
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 3 for T-cell epitope mapping

<400> 126
 Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala
 1 5 10 15
 Leu Glu Glu Leu
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<210> 127
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 <220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 4 for T-cell epitope mapping

 <400> 127
 Glu Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp
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 Leu Gly Ser Ala .
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<210> 128
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 <400> 128
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 Asn His Val Asn
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<210> 129
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<210> 130
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<210> 131
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Gly Leu Glu Phe
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9 for T-cell epitope mapping

<400> 132
Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr
1 5 10 15

Tyr Ile Pro Val
20

<210> 133
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
10 for T-cell epitope mapping

<400> 133
Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe
1 5 10 15

Gln Ala Pro Phe
20

<210> 134
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
11 for T-cell epitope mapping

<400> 134

Ala	Ala	Phe	Gln	Ala	Pro	Phe	Cys	Ala	Gly	Ala	Met	Ala	Val	Val	Gly
1				5					10				15		

Gly	Ala	Leu	Ala
			20

<210> 135
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
12 for T-cell epitope mapping

<400> 135

Val	Val	Gly	Gly	Ala	Leu	Ala	Tyr	Leu	Val	Val	Lys	Thr	Leu	Ile	Asn
1				5					10				15		

Ala	Thr	Gln	Leu
			20

<210> 136
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
13 for T-cell epitope mapping

<400> 136

Leu	Ile	Asn	Ala	Thr	Gln	Leu	Leu	Lys	Leu	Leu	Ala	Lys	Leu	Ala	Glu
1				5					10				15		

Leu	Val	Ala	Ala
			20

<210> 137
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
14 for T-cell epitope mapping

<400> 137
 Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
 1 5 10 15
 Ala Asp Ile Ile
 20

<210> 138
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 15 for T-cell epitope mapping

<400> 138
 Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu
 1 5 10 15
 Phe Ile Thr Asn
 20

<210> 139
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 16 for T-cell epitope mapping

<400> 139
 Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp
 1 5 10 15
 Asp Lys Leu Thr
 20

<210> 140
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 17 for T-cell epitope mapping

<400> 140
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 1 5 10 15
 Gly Trp Ser Asn
 20

<210> 141
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
18 for T-cell epitope mapping

<400> 141
Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro
1 5 10 15
Gly Leu Thr Gly
20

<210> 142
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
19 for T-cell epitope mapping

<400> 142
Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr
1 5 10 15
Gly Leu Phe Gly
20

<210> 143
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
20 for T-cell epitope mapping

<400> 143
Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly
1 5 10 15
Leu Ala His Ala
20

<210> 144
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
21 for T-cell epitope mapping

<400> 144

Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu
1 5 10 15

Pro Ala Leu Ala
20

<210> 145

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
22 for T-cell epitope mapping

<400> 145

Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly
1 5 10 15

Gly Leu Pro Ser
20

<210> 146

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
23 for T-cell epitope mapping

<400> 146

Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr
1 5 10 15

Arg Gln Ala Leu
20

<210> 147

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide
24 for T-cell epitope mapping

<400> 147

Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly
1 5 10 15

Ala Ala Ala Glu
20

<210> 148
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
25 for T-cell epitope mapping

<400> 148
Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val
1 5 10 15
Ser Ala Gln Gly
20

<210> 149
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
26 for T-cell epitope mapping

<400> 149
Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
1 5 10 15
Met Gly Gly

<210> 150
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
27 for T-cell epitope mapping

<400> 150
Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly
1 5 10 15
Thr Thr Thr Lys
20

<210> 151
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
28 for T-cell epitope mapping

<400> 151
 Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly
 1 5 10 15

Thr Glu Asp Ala
 20

<210> 152
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 29 for T-cell epitope mapping

<400> 152
 Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala
 1 5 10 15

Gly Gly Gly Gln
 20

<210> 153
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HTCC#1 peptide
 30 for T-cell epitope mapping

<400> 153
 Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val
 1 5 10 15

Arg Asn Val Val
 20

<210> 154
 <211> 84
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> secreted form of DPPD

<400> 154
 Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro
 1 5 10 15

Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys
 20 25 30

Tyr Pro Asp Gly Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr
 35 40 45

Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro
 50 55 60

Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln
 65 70 75 80

Pro Asn Ala Pro

<210> 155
 <211> 2836
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb9.9A (MTI-A)

<220>
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 <223> n = g, a, c or t

<400> 155
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 cgattacccc cacggaaagg acgacgatcg ttcgtttgct cggtcagtcg tacttggcga 180
 cgggcatggc gcggtttctt acctcgatcg cacagcagct gaccttcggc ccagggggca 240
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 gccggcggtt gtcggcgagt ttggcgcggg cggagccggt cgggaggttg tcggtgccgc 360
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 cggccgcggc tgctccaacc accggagtag tgcccgagc cgccgatgaa gtatcagcgc 1140
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tccaatgact ggctaaacga gcacccgggg atggcgggtca tgcgcgagca gggcattgtc 2340
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attcggcacg aggcacgagg cgggtgtcgg gacgacggga tcgatcacga tcatcgaccg 2760
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<210> 156
<211> 15
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
      ORF peptide

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<400> 156
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala
  1             5             10             15

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<210> 157
<211> 15
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
      ORF peptide

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<400> 157
Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
  1             5             10             15

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```

<210> 158
<211> 15
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
      ORF peptide

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<400> 158
Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
  1             5             10             15

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```

<210> 159
<211> 15
<212> PRT
<213> Artificial Sequence

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<220>
 <223> Description of Artificial Sequence:MtB9.9A (MTI-A)
 ORF peptide

<400> 159
 Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala
 1 5 10 15

<210> 160
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:MtB9.9A (MTI-A)
 ORF peptide

<400> 160
 Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val
 1 5 10 15

<210> 161
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:MtB9.9A (MTI-A)
 ORF peptide

<400> 161
 Ala Glu His Gln Ala Ile Val Arg Asp Val Leu Ala Ala Gly Asp
 1 5 10 15

<210> 162
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:MtB9.9A (MTI-A)
 ORF peptide

<400> 162
 Ile Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala
 1 5 10 15

<210> 163
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:MtB9.9A (MTI-A)
 ORF peptide

<400> 163

Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln
1 5 10 15

<210> 164

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 164

Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr
1 5 10 15

<210> 165

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 165

Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn
1 5 10 15

<210> 166

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 166

Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu
1 5 10 15

Gln Ala

<210> 167

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 167

Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln
1 5 10 15

<210> 168

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 168

Ile Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala
1 5 10 15

<210> 169

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 169

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala
1 5 10 15

<210> 170

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 170

Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala
1 5 10 15

<210> 171

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 171

Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
1 5 10 15

<210> 172
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 172
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln
1 5 10 15

<210> 173
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 173
Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
1 5 10 15

<210> 174
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 174
Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
1 5 10 15

<210> 175
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 175
Ser Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly
1 5 10 15

<210> 176
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 176
Lys Ala Gly Leu Met His Thr Ile Gly Gln Ala Glu Gln Ala
1 5 10

<210> 177
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 177
Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala Met Ser Ala Gln
1 5 10 15

<210> 178
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 178
Gln Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly
1 5 10 15

<210> 179
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 179
Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala
1 5 10 15

<210> 180
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 180
 Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His
 1 5 10 15

<210> 181
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Mtb9.8 ORF
 peptide

<400> 181
 Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala
 1 5 10 15

<210> 182
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Mtb9.8 ORF
 peptide

<400> 182
 Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val
 1 5 10 15

<210> 183
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Mtb9.8 ORF
 peptide

<400> 183
 Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu Leu Asp
 1 5 10 15

<210> 184
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Mtb9.8 ORF
 peptide

<400> 184
 Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn
 1 5 10 15

<210> 185
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 185
Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
1 5 10 15

<210> 186
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 186
Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala
1 5 10 15

Asp Ala

<210> 187
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer PDM-294

<400> 187
cgtaatcacg tgcagaagta cggcggatc 29

<210> 188
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer PDM-295

<400> 188
ccgactagaa ttcactattg acaggcccat c 31

<210> 189
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-268

 <400> 189
 ctaagtagta ctgatcggt gtcggtgggc 30

 <210> 190
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-296

 <400> 190
 catcgatagg cctggccgca tcgtcacc 28

 <210> 191
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-157

 <400> 191
 ctagttagta ctcagtcgca gaccgtg 27

 <210> 192
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-160

 <400> 192
 gcagtgcga attcacttcg actcc 25

 <210> 193
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-69

 <400> 193
 ggatccagcg ctgagatgaa gaccgatgcc gct 33

<210> 194
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-83

 <400> 194
 ggatatctgc agaattcagg tttaaagccc atttgcca 38

 <210> 195
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-192

 <400> 195
 tgtggctcga aaccaccgag cggttc 26

 <210> 196
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer PDM-60

 <400> 196
 gagagaattc tcagaagccc atttgcgagg aca 33

 <210> 197
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 oligonucleotide 5' primer

 <400> 197
 caattacata tgcataacca tcaccatcac atgagcagag cgttcatcat c 51

 <210> 198
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 oligonucleotide 3' primer

<400> 198
 catggaattc gccgttagac gacgtttcgt a 31

<210> 199
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification oligonucleotide 5' primer

<400> 199
 caattacata tgcatacaca tcaccatcac acggccgcgt ccgataactt c 51

<210> 200
 <211> 33
 <212> DNA
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 amplification oligonucleotide 3' primer

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<220>
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ttg tac gac ctt ctg ggg att gga ata ccc aac caa ggg ggt atc ctt 96
 Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
 20 25 30

tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag gag ctg gca gca 144
 Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35 40 45

gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg gac aaa tac gcc 192
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60

ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa ctg gca gac ctc 240
 Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80

gat cgt cag ctc atc agc ctg atc cac gac cag gcc aac gcg gtc cag	288
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln	
85 90 95	
acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt ctc gag ttc gtg	336
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val	
100 105 110	
cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc gtc ggg cac gcc	384
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala	
115 120 125	
cta tcg gcc gcc ttc cag gcg ccg ttt tgc gcg ggc gcg atg gcc gta	432
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val	
130 135 140	
gtg ggc ggc gcg ctt gcc tac ttg gtc gtg aaa acg ctg atc aac gcg	480
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala	
145 150 155 160	
act caa ctc ctc aaa ttg ctt gcc aaa ttg gcg gag ttg gtc gcg gcc	528
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala	
165 170 175	
gcc att gcg gac atc att tcg gat gtg gcg gac atc atc aag ggc atc	576
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile	
180 185 190	
ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa	624
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys	
195 200 205	
gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga	672
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg	
210 215 220	
ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc	720
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr	
225 230 235 240	
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Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala	
245 250 255	
ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc	816
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser	
260 265 270	
tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt	864
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe	
275 280 285	
ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg cag	912
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln	
290 295 300	
gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag	960
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln	
305 310 315 320	

gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg 1008
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335

ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg 1056
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350

aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act 1104
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 355 360 365

gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa 1152
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 370 375 380

aag gtg ctg gta cga aac gtc gtc taa 1179
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 Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35 40 45
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60
 Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80
 Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95
 Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
 100 105 110
 Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 120 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175

Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile
 180 185 190
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 370 375 380
 Lys Val Leu Val Arg Asn Val Val
 385 390